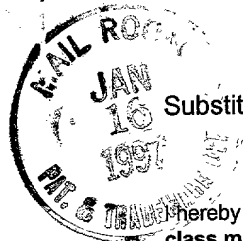


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Attorney Docket Number: 00786/345001

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Additional names attached: NO

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Boston, MA 02114

Additional names/addresses attached: NO

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Execution Date: November 15, 1996

4. Application numbers or patent numbers:

A. Patent Application Numbers:

08/717,294

B. Patent Numbers:

5. Name and address of party to whom correspondence concerning document should be mailed:

Karen Lech Elbing, Reg. No. 35,238  
Clark & Elbing LLP  
585 Commercial Street  
Boston, MA 02109

6. Total number of applications/patents involved: 1

7. Total fee (37 CFR 3.41): \$40.00

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KAREN LECH ELBING  
Name of person signing

Karen Lech Elbing  
Signature

13 January 1997  
Date

## ASSIGNMENT

For valuable consideration, we, Brian Seed, of Boston, Massachusetts; and Jurgen Haas of Schriesheim, Germany hereby assign to THE GENERAL HOSPITAL CORPORATION, a MASSACHUSETTS corporation having a place of business at 55 Fruit Street, Boston, MA 02114, and its successors and assigns (collectively hereinafter called "the Assignee"), the entire right, title and interest throughout the world in the inventions and improvements which are subject of an application for United States Patent signed by us, entitled HIGH LEVEL EXPRESSION OF PROTEINS, filed September 20, 1996, and assigned U.S. Serial Number 08/717,294, and we authorize and request the attorneys appointed in said application to hereafter complete this assignment by inserting above the filing date and serial number of said application when known; this assignment including said application, any and all United States and foreign patents, utility models, and design registrations granted for any of said inventions or improvements, and the right to claim priority based on the filing date of said application under the International Convention for the Protection of Industrial Property, the Patent Cooperation Treaty, the European Patent Convention, and all other treaties of like purposes; and we authorize the Assignee to apply in all countries in our name or in its own name for patents, utility models, and design registrations and like rights of exclusion and for inventors' certificates for said inventions and improvements; and we agree for ourselves and our respective heirs, legal representatives and assigns, without further compensation to perform such lawful acts and to sign such further applications, assignments, Preliminary Statements and other lawful documents as the Assignee may reasonably request to effectuate fully this assignment.

IN WITNESS WHEREOF, I hereto set my hand and seal at Boston, Massachusetts,  
this 15<sup>th</sup> day of November, 1996

Brian Seed L.S.  
BRIAN SEED

STATE OF Massachusetts:  
:SS.  
COUNTY OF Suffolk:

Before me this 15 day of November, 1996, personally appeared

Brian Seed known to me to be the person whose name is subscribed to the foregoing Assignment, and acknowledged that he/she executed the same as his/her free act and deed for the purposes therein contained.

Martha K. Leonard  
Notary Public

My Commission Expires: 12/13/96

[Notary's Seal Here]



IN WITNESS WHEREOF, I hereto set my hand and seal at \_\_\_\_\_,

this \_\_\_\_\_ day of \_\_\_\_\_, 19\_\_

L.S.

## JURGEN HAAS

STATE OF \_\_\_\_\_:

**:SS.**

COUNTY OF \_\_\_\_\_:

Before me this \_\_\_\_\_ day of \_\_\_\_\_, 19\_\_\_\_, personally appeared

\_\_\_\_\_ known to me to be the person whose name is subscribed to the foregoing Assignment, and acknowledged that he/she executed the same as his/her free act and deed for the purposes therein contained.

**Notary Public**

My Commission Expires:

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**210211.B11**



PATENT  
ATTORNEY DOCKET NO.00786/345001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Brian Seed et al.  
Serial No.: 08/717,294  
Filed : September 20, 1996  
Title : HIGH LEVEL EXPRESSION OF PROTEINS

Art Unit:  
Examiner:

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Effective immediately, please change the address in the above matter to:

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(617) 723-4197 at the new address. The telephone and facsimile numbers are: (617) 723-6777  
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Brian Seed et al.  
Serial No.: 08/717,294  
Filed : September 20, 1996  
Title : HIGH LEVEL EXPRESSION OF PROTEINS

Art Unit:  
Examiner:

Assistant Commissioner of Patents and Trademarks  
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PETITION UNDER 37 CFR §1.47

Applicants hereby submit this petition under 37 CFR §1.47. As stated in the accompanying Declarations of Dr. Brian Seed and Ms. Susan M. Cuffe, one of the inventors of the above-identified patent application, Jurgen Haas, cannot be reached despite diligent effort, and applicants request that this application be considered complete even in the absence of his signature on an oath or declaration. As stated in the accompanying Declarations, the last known address of Dr. Haas was Huberweg 13, 69198 Schriesheim, Germany.

Submitted herewith is a check for the required fee under 37 CFR § 1.17(h).

Date: 13 January 1997

Karen Lech Elbing  
Karen Lech Elbing, Ph.D.  
Reg. No. 35,238

Clark & Elbing LLP  
585 Commercial Street  
Boston, MA 02109-1024  
Telephone: (617) 723-6777  
Facsimile: (617) 723-8962  
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Brian Seed et al.  
Serial No.: 08/717,294  
Filed : September 20, 1996  
Title : HIGH LEVEL EXPRESSION OF PROTEINS

Art Unit:  
Examiner:

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RESPONSE TO NOTICE TO FILE MISSING PARTS OF APPLICATION

Responsive to the Notice to File Missing Parts of Application under 37 CFR 1.53(d)  
mailed November 12, 1996 (a copy of which is enclosed), Applicant as a large entity submits  
herewith the following:

A Combined Declaration and Power of Attorney in compliance with 37 CFR 1.63.

Payment of the surcharge of \$130.00 for late filing of the declaration.

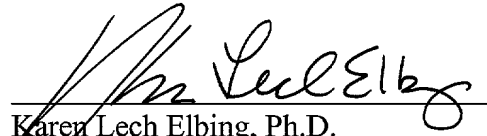
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Lisa Fothergill

960260-462480

It is understood that this perfects the application and no additional papers or filing fees are required. If there are any other charges, or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

  
Karen Lech Elbing, Ph.D.  
Reg. No. 35,238

Date: 13 January 1997

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Telephone: 617-723-6777  
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FREDERICK P. FISH  
(1855-1930)

W.K. RICHARDSON  
(1859-1951)

# **FISH & RICHARDSON P.C.**

225 FRANKLIN STREET  
BOSTON, MASSACHUSETTS 02110-2804 MA

TELEPHONE: 617/542-5070

FAX: 617/542-8906

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September 20, 1996

Attorney Docket No.: 00786/345001

## **BOX PATENT APPLICATION**

Commissioner of Patents and Trademarks  
Washington, DC 20231

Presented for filing is a new original patent application of:

Applicant: **BRIAN SEED AND JORGEN HAAS**

Title : **HIGH LEVEL EXPRESSION OF PROTEINS**

Enclosed are the following papers, including all those required for a filing date under 37 CFR §1.53(b):

Pages of Specification	67
Pages of Claims	4
Pages of Abstract	1
Signed Declaration	[To Be Filed At A Later Date]
Sheets of Drawing	18

Basic filing fee	750.00
Total claims in excess of 20 times \$22.00	176.00
Independent claims in excess of 3 times \$78.00	0.00
Multiple dependent claims	0.00
Total filing fee:	\$ 926.00

A check for the filing fee is enclosed. Please charge any other required fees, or apply any credits, to Deposit Account No. 06-1050, referencing the Attorney Docket number shown above.

If this application is found to be INCOMPLETE, or if it appears that a telephone conference would helpfully advance prosecution, please telephone the undersigned at 617/542-5070.

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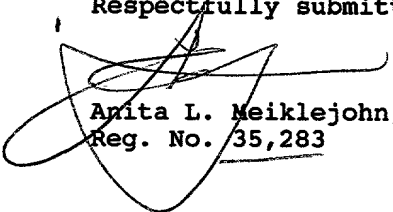
Lisa G Gray  
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BOX PATENT APPLICATION  
September 20, 1996  
Page 2

Kindly acknowledge receipt of this application by returning the enclosed postcard.

Respectfully submitted,



Anita L. Meiklejohn, Ph.D.  
Reg. No. 35,283

Enclosures

03747244-09096  
950360-46247288



**APPLICATION**  
**FOR**  
**UNITED STATES LETTERS PATENT**

**TITLE:** **HIGH LEVEL EXPRESSION OF PROTEINS**

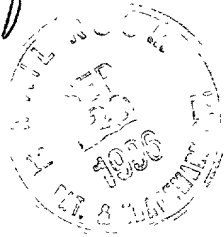
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Tina G. Gray  
Lisa G. Gray



HIGH LEVEL EXPRESSION OF PROTEINS

Field of the Invention

5           The invention concerns genes and methods for  
expressing eukaryotic and viral proteins at high levels in  
eukaryotic cells.

Background of the Invention

Expression of eukaryotic gene products in  
10 prokaryotes is sometimes limited by the presence of codons  
that are infrequently used in *E. coli*. Expression of such  
genes can be enhanced by systematic substitution of the  
endogenous codons with codons over represented in highly  
expressed prokaryotic genes (Robinson et al., Nucleic Acids  
15 Res. 12:6663, 1984). It is commonly supposed that rare  
codons cause pausing of the ribosome, which leads to a  
failure to complete the nascent polypeptide chain and a  
uncoupling of transcription and translation. Pausing of the  
ribosome is thought to lead to exposure of the 3' end of the  
20 mRNA to cellular ribonucleases.

Summary of the Invention

The invention features a synthetic gene encoding a  
protein normally expressed in a mammalian cell or other  
eukaryotic cell wherein at least one non-preferred or less  
25 preferred codon in the natural gene encoding the protein has  
been replaced by a preferred codon encoding the same amino  
acid.

Preferred codons are: Ala (gcc); Arg (cgc); Asn  
(aac); Asp (gac) Cys (tgc); Gln (cag); Gly (ggc); His (cac);  
30 Ile (atc); Leu (ctg); Lys (aag); Pro (ccc); Phe (ttc); Ser  
(agc); Thr (acc); Tyr (tac); and Val (gtg). Less preferred  
codons are: Gly (ggg); Ile (att); Leu (ctc); Ser (tcc); Val  
(gtc); and Arg (agg). All codons which do not fit the  
description of preferred codons or less preferred codons are

non-preferred codons. In general, the degree of preference of a particular codon is indicated by the prevalence of the codon in highly expressed human genes as indicated in Table 1 under the heading "High." For example, "atc" represents 77% of the Ile codons in highly expressed mammalian genes and is the preferred Ile codon; "att" represents 18% of the Ile codons in highly expressed mammalian genes and is the less preferred Ile codon. The sequence "ata" represents only 5% of the Ile codons in highly expressed human genes as is a non-preferred Ile codon. Replacing a codon with another codon that is more prevalent in highly expressed human genes will generally increase expression of the gene in mammalian cells. Accordingly, the invention includes replacing a less preferred codon with a preferred codon as well as replacing a non-preferred codon with a preferred or less preferred codon.

By "protein normally expressed in a mammalian cell" is meant a protein which is expressed in mammalian under natural conditions. The term includes genes in the mammalian genome such as those encoding Factor VIII, Factor IX, interleukins, and other proteins. The term also includes genes which are expressed in a mammalian cell under disease conditions such as oncogenes as well as genes which are encoded by a virus (including a retrovirus) which are expressed in mammalian cells post-infection. By "protein normally expressed in a eukaryotic cell" is meant a protein which is expressed in a eukaryote under natural conditions. The term also includes genes which are expressed in a mammalian cell under disease conditions.

In preferred embodiments, the synthetic gene is capable of expressing the mammalian or eukaryotic protein at a level which is at least 110%, 150%, 200%, 500%, 1,000%, 5,000% or even 10,000% of that expressed by the "natural"

(or "native") gene in an *in vitro* mammalian cell culture system under identical conditions (i.e., same cell type, same culture conditions, same expression vector).

Suitable cell culture systems for measuring  
5 expression of the synthetic gene and corresponding natural gene are described below. Other suitable expression systems employing mammalian cells are well known to those skilled in the art and are described in, for example, the standard molecular biology reference works noted below. Vectors  
10 suitable for expressing the synthetic and natural genes are described below and in the standard reference works described below. By "expression" is meant protein expression. Expression can be measured using an antibody specific for the protein of interest. Such antibodies and  
15 measurement techniques are well known to those skilled in the art. By "natural gene" and "native gene" is meant the gene sequence (including naturally occurring allelic variants) which naturally encodes the protein, i.e., the native or natural coding sequence.

20 In other preferred embodiments at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the codons in the natural gene are non-preferred codons.

In other preferred embodiments at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the non-preferred  
25 codons in the natural gene are replaced with preferred codons or less preferred codons.

In other preferred embodiments at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the non-preferred  
30 codons in the natural gene are replaced with preferred codons.

In a preferred embodiment the protein is a retroviral protein. In a more preferred embodiment the protein is a lentiviral protein. In an even more preferred

embodiment the protein is an HIV protein. In other preferred embodiments the protein is gag, pol, env, gp120, or gp160. In other preferred embodiments the protein is a human protein. In more preferred embodiments, the protein is human Factor VIII and the protein in B region deleted human Factor VIII. In another preferred embodiment the protein is green fluorescent protein.

In various preferred embodiments at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, and 95% of the codons in the synthetic gene are preferred or less preferred codons.

The invention also features an expression vector comprising the synthetic gene.

In another aspect the invention features a cell harboring the synthetic gene. In various preferred embodiments the cell is a prokaryotic cell and the cell is a mammalian cell.

In preferred embodiments the synthetic gene includes fewer than 50, fewer than 40, fewer than 30, fewer than 20, fewer than 10, fewer than 5, or no "cg" sequences.

The invention also features a method for preparing a synthetic gene encoding a protein normally expressed by a mammalian cell or other eukaryotic cell. The method includes identifying non-preferred and less-preferred codons in the natural gene encoding the protein and replacing one or more of the non-preferred and less-preferred codons with a preferred codon encoding the same amino acid as the replaced codon.

Under some circumstances (e.g., to permit introduction of a restriction site) it may be desirable to replace a non-preferred codon with a less preferred codon rather than a preferred codon.

It is not necessary to replace all less preferred or non-preferred codons with preferred codons. Increased

expression can be accomplished even with partial replacement of less preferred or non-preferred codons with preferred codons. Under some circumstances it may be desirable to only partially replace non-preferred codons with preferred or less preferred codons in order to obtain an intermediate level of expression.

In other preferred embodiments the invention features vectors (including expression vectors) comprising one or more the synthetic genes.

By "vector" is meant a DNA molecule, derived, e.g., from a plasmid, bacteriophage, or mammalian or insect virus, into which fragments of DNA may be inserted or cloned. A vector will contain one or more unique restriction sites and may be capable of autonomous replication in a defined host or vehicle organism such that the cloned sequence is reproducible. Thus, by "expression vector" is meant any autonomous element capable of directing the synthesis of a protein. Such DNA expression vectors include mammalian plasmids and viruses.

The invention also features synthetic gene fragments which encode a desired portion of the protein. Such synthetic gene fragments are similar to the synthetic genes of the invention except that they encode only a portion of the protein. Such gene fragments preferably encode at least 50, 100, 150, or 500 contiguous amino acids of the protein.

In constructing the synthetic genes of the invention it may be desirable to avoid CpG sequences as these sequences may cause gene silencing. Thus, in a preferred embodiment the coding region of the synthetic gene does not include the sequence "cg."

The codon bias present in the HIV gp120 env gene is also present in the gag and pol genes. Thus, replacement of a portion of the non-preferred and less preferred codons

found in these genes with preferred codons should produce a gene capable of higher level expression. A large fraction of the codons in the human genes encoding Factor VIII and Factor IX are non-preferred codons or less preferred codons.

- 5 Replacement of a portion of these codons with preferred codons should yield genes capable of higher level expression in mammalian cell culture.

The synthetic genes of the invention can be introduced into the cells of a living organism. For  
10 example, vectors (viral or non-viral) can be used to introduce a synthetic gene into cells of a living organism for gene therapy.

Conversely, it may be desirable to replace preferred codons in a naturally occurring gene with less-preferred  
15 codons as a means of lowering expression.

Standard reference works describing the general principles of recombinant DNA technology include Watson et al., Molecular Biology of the Gene, Volumes I and II, the Benjamin/Cummings Publishing Company, Inc., publisher, Menlo  
20 Park, CA (1987); Darnell et al., Molecular Cell Biology, Scientific American Books, Inc., Publisher, New York, N.Y. (1986); Old et al., Principles of Gene Manipulation: An Introduction to Genetic Engineering, 2d edition, University of California Press, publisher, Berkeley, CA (1981);  
25 Maniatis et al., Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory, publisher, Cold Spring Harbor, NY (1989); and Current Protocols in Molecular Biology, Ausubel et al., Wiley Press, New York, NY (1992).

By "transformed cell" is meant a cell into which (or  
30 into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a selected DNA molecule, e.g., a synthetic gene.

By "positioned for expression" is meant that a DNA molecule, e.g., a synthetic gene, is positioned adjacent to a DNA sequence which directs transcription and translation of the sequence (i.e., facilitates the production of the protein encoded by the synthetic gene.

#### Description of the Drawings

Figure 1 depicts the sequence of the synthetic gp120 and a synthetic gp160 gene in which codons have been replaced by those found in highly expressed human genes.

Figure 2 is a schematic drawing of the synthetic gp120 (HIV-1 MN) gene. The shaded portions marked v1 to v5 indicate hypervariable regions. The filled box indicates the CD4 binding site. A limited number of the unique restriction sites are shown: H (Hind3), Nh (Nhe1), P (Pst1), Na (Nae1), M (Mlu1), R (EcoR1), A (Age1) and No (Not1). The chemically synthesized DNA fragments which served as PCR templates are shown below the gp120 sequence, along with the locations of the primers used for their amplification.

Figure 3 is a photograph of the results of transient transfection assays used to measure gp120 expression. Gel electrophoresis of immunoprecipitated supernatants of 293T cells transfected with plasmids expressing gp120 encoded by the IIIB isolate of HIV-1 (gp120IIIB), by the MN isolate of HIV-1 (gp120mn), by the MN isolate of HIV-1 modified by substitution of the endogenous leader peptide with that of the CD5 antigen (gp120mnCD5L), or by the chemically synthesized gene encoding the MN variant of HIV-1 with the human CD5Leader (syngp120mn). Supernatants were harvested following a 12 hour labeling period 60 hours post-transfection and immunoprecipitated with CD4:IgG1 fusion protein and protein A sepharose.

Figure 4 is a graph depicting the results of ELISA assays used to measure protein levels in supernatants of transiently transfected 293T cells. Supernatants of 293T cells transfected with plasmids expressing gp120 encoded by the IIIB isolate of HIV-1 (gp120 IIIB), by the MN isolate of HIV-1 (gp120mn), by the MN isolate of HIV-1 modified by substitution of the endogenous leader peptide with that of CD5 antigen (gp120mn CD5L), or by the chemically synthesized gene encoding the MN variant of HIV-1 with human CDS leader (syngp120mn) were harvested after 4 days and tested in a gp120/CD4 ELISA. The level of gp120 is expressed in ng/ml.

Figure 5A is a photograph of a gel illustrating the results of an immunoprecipitation assay used to measure expression of the native and synthetic gp120 in the presence of rev in trans and the RRE in cis. In this experiment 293T cells were transiently transfected by calcium phosphate coprecipitation of 10  $\mu$ g of plasmid expressing: (A) the synthetic gp120MN sequence and RRE in cis, (B) the gp120 portion of HIV-1 IIIB, (C) the gp120 portion of HIV-1 IIIB and RRE in cis, all in the presence or absence of rev expression. The RRE constructs gp120IIIBRRE and syngp120mnRRE were generated using an EagI/HpaI RRE fragment cloned by PCR from a HIV-1 HXB2 proviral clone. Each gp120 expression plasmid was cotransfected with 10  $\mu$ g of either pCMVrev or CDM7 plasmid DNA. Supernatants were harvested 60 hours post transfection, immunoprecipitated with CD4:IgG fusion protein and protein A agarose, and run on a 7% reducing SDS-PAGE. The gel exposure time was extended to allow the induction of gp120IIIBrre by rev to be demonstrated.

Figure 5B is a shorter exposure of a similar experiment in which syngp120mnrrre was cotransfected with or without pCMVrev.

Figure 5C is a schematic diagram of the constructs used in Figure 5A.

Figure 6 is a comparison of the sequence of the wild-type ratTHY-1 gene (wt) and a synthetic ratTHY-1 gene (env) constructed by chemical synthesis and having the most prevalent codons found in the HIV-1 env gene.

Figure 7 is a schematic diagram of the synthetic ratTHY-1 gene. The solid black box denotes the signal peptide. The shaded box denotes the sequences in the precursor which direct the attachment of a phosphatidyl-inositol glycan anchor. Unique restriction sites used for assembly of the THY-1 constructs are marked H (Hind3), M (Mlu1), S (Sac1) and No (Not1). The position of the synthetic oligonucleotides employed in the construction are shown at the bottom of the figure.

Figure 8 is a graph depicting the results of flow cytometry analysis. In this experiment 293T cells transiently transfected with either a wild-type ratTHY-1 expression plasmid (thick line), ratTHY-1 with envelope codons expression plasmid (thin line), or vector only (dotted line) by calcium phosphate co-precipitation. Cells were stained with anti-ratTHY-1 monoclonal antibody OX7 followed by a polyclonal FITC-conjugated anti-mouse IgG antibody 3 days after transfection.

Figure 9A is a photograph of a gel illustrating the results of immunoprecipitation analysis of supernatants of human 293T cells transfected with either syngp120mn (A) or a construct syngp120mn.rTHY-1env which has the rTHY-1env gene in the 3' untranslated region of the syngp120mn gene (B). The syngp120mn.rTHY-1env construct was generated by inserting a Not1 adapter into the blunted Hind3 site of the rTHY-1env plasmid. Subsequently, a 0.5 kb Not1 fragment containing the rTHY-1env gene was cloned into the Not1 site

of the syngp120mn plasmid and tested for correct orientation. Supernatants of <sup>35</sup>S labeled cells were harvested 72 hours post transfection, precipitated with CD4:IgG fusion protein and protein A agarose, and run on a 7% reducing SDS-PAGE.

Figure 9B is a schematic diagram of the constructs used in the experiment depicted in Figure 9A.

Figure 10A is a photograph of COS cells transfected with vector only showing no GFP fluorescence.

Figure 10B is a photograph of COS cells transfected with a CDM7 expression plasmid encoding native GFP engineered to include a consensus translational initiation sequence.

Figure 10C is a photograph of COS cells transfected with an expression plasmid having the same flanking sequences and initiation consensus as in Figure 10B, but bearing a codon optimized gene sequence.

Figure 10D is a photograph of COS cells transfected with an expression plasmid as in Figure 10C, but bearing a Thr at residue 65 in place of Ser.

Figure 11 depicts the sequence of a synthetic gene encoding green fluorescent proteins (SEQ ID NO:40).

Figure 12 depicts the sequence of a native human Factor VIII gene lacking the central B domain (amino acids 760-1639, inclusive) (SEQ ID NO:41).

Figure 13 depicts the sequence of a synthetic human Factor VIII gene lacking the central B domain (amino acids 760-1639, inclusive) (SEQ ID NO:42).

## Description of the Preferred Embodiments

### EXAMPLE 1

#### Construction of a Synthetic gp120 Gene Having Codons Found in Highly Expressed Human Genes

5           A codon frequency table for the envelope precursor of the LAV subtype of HIV-1 was generated using software developed by the University of Wisconsin Genetics Computer Group. The results of that tabulation are contrasted in Table 1 with the pattern of codon usage by a collection of  
10 highly expressed human genes. For any amino acid encoded by degenerate codons, the most favored codon of the highly expressed genes is different from the most favored codon of the HIV envelope precursor. Moreover a simple rule describes the pattern of favored envelope codons wherever it  
15 applies: preferred codons maximize the number of adenine residues in the viral RNA. In all cases but one this means that the codon in which the third position is A is the most frequently used. In the special case of serine, three codons equally contribute one A residue to the mRNA;  
20 together these three comprise 85% of the serine codons actually used in envelope transcripts. A particularly striking example of the A bias is found in the codon choice for arginine, in which the AGA triplet comprises 88% of the arginine codons. In addition to the preponderance of A  
25 residues, a marked preference is seen for uridine among degenerate codons whose third residue must be a pyrimidine. Finally, the inconsistencies among the less frequently used variants can be accounted for by the observation that the dinucleotide CpG is under represented; thus the third  
30 position is less likely to be G whenever the second position is C, as in the codons for alanine, proline, serine and threonine; and the CGX triplets for arginine are hardly used at all.

**TABLE 1:** Codon Frequency in the HIV-1 IIIb env gene and in highly expressed human genes.

		High Env		High Env	
5	<u>Ala</u>			<u>Cys</u>	
	GC	C	53	TG	C
		T	17		T
		A	13		
10		G	17		
	<u>Arg</u>			<u>Gln</u>	
	CG	C	37	CA	A
		T	7		G
15		A	6		
		G	21	<u>Glu</u>	
	AG	A	10	GA	A
		G	18		G
20					
	<u>Asn</u>			<u>Gly</u>	
	AA	C	78	GG	C
		T	22		T
25					A
	<u>Asp</u>				
	GA	C	75	<u>His</u>	
		T	25	CA	C
30					T
	<u>Leu</u>			<u>Ile</u>	
	CT	C	26	AT	C
		T	5		T
35		A	3		A
		G	58	<u>Ser</u>	
	TT	A	2	TC	C
		G	6		T
40					A
	<u>Lys</u>				G
	AA	A	18	<u>Thr</u>	
		G	82	AC	C
					T
	<u>Pro</u>				A
	CC	C	48		G
		T	19	<u>Tyr</u>	
		A	16	TA	C
					T

G 17 5

Phe

TT	C	80	26
	T	20	74

Val

GT	C	25	12
	T	7	9
	A	5	62
	G	64	18

5

10 Codon frequency was calculated using the GCG program established the University of Wisconsin Genetics Computer Group. Numbers represent the percentage of cases in which the particular codon is used. Codon usage frequencies of envelope genes of other HIV-1 virus isolates are comparable and show a similar bias.

15 In order to produce a gp120 gene capable of high level expression in mammalian cells, a synthetic gene encoding the gp120 segment of HIV-1 was constructed (syngp120mn), based on the sequence of the most common North American subtype, HIV-1 MN (Shaw et al., Science 226:1165, 20 1984; Gallo et al., Nature 321:119, 1986). In this synthetic gp120 gene nearly all of the native codons have been systematically replaced with codons most frequently used in highly expressed human genes (Figure 1). This synthetic gene was assembled from chemically synthesized 25 oligonucleotides of 150 to 200 bases in length. If oligonucleotides exceeding 120 to 150 bases are chemically synthesized, the percentage of full-length product can be low, and the vast excess of material consists of shorter oligonucleotides. Since these shorter fragments inhibit 30 cloning and PCR procedures, it can be very difficult to use oligonucleotides exceeding a certain length. In order to use crude synthesis material without prior purification, single-stranded oligonucleotide pools were PCR amplified before cloning. PCR products were purified in agarose gels 35 and used as templates in the next PCR step. Two adjacent

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fragments could be co-amplified because of overlapping sequences at the end of either fragment. These fragments, which were between 350 and 400 bp in size, were subcloned into a pCDM7-derived plasmid containing the leader sequence of the CD5 surface molecule followed by a Nhe1/Pst1/Mlu1/EcoR1/BamH1 polylinker. Each of the restriction enzymes in this polylinker represents a site that is present at either the 5' or 3' end of the PCR-generated fragments. Thus, by sequential subcloning of each of the 4 long fragments, the whole gp120 gene was assembled. For each fragment three to six different clones were subcloned and sequenced prior to assembly. A schematic drawing of the method used to construct the synthetic gp120 is shown in Figure 2. The sequence of the synthetic gp120 gene (and a synthetic gp160 gene created using the same approach) is presented in Figure 1.

The mutation rate was considerable. The most commonly found mutations were short (1 nucleotide) and long (up to 30 nucleotides) deletions. In some cases it was necessary to exchange parts with either synthetic adapters or pieces from other subclones without mutation in that particular region. Some deviations from strict adherence to optimized codon usage were made to accommodate the introduction of restriction sites into the resulting gene to facilitate the replacement of various segments (Figure 2). These unique restriction sites were introduced into the gene at approximately 100 bp intervals. The native HIV leader sequence was exchanged with the highly efficient leader peptide of the human CD5 antigen to facilitate secretion (Aruffo et al., *Cell* 61:1303, 1990) The plasmid used for construction is a derivative of the mammalian expression vector pCDM7 transcribing the inserted gene under the control of a strong human CMV immediate early promoter.

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To compare the wild-type and synthetic gp120 coding sequences, the synthetic gp120 coding sequence was inserted into a mammalian expression vector and tested in transient transfection assays. Several different native gp120 genes were used as controls to exclude variations in expression levels between different virus isolates and artifacts induced by distinct leader sequences. The gp120 HIV IIIb construct used as control was generated by PCR using a Sall/Xho1 HIV-1 HXB2 envelope fragment as template. To exclude PCR induced mutations, a Kpn1/Ear1 fragment containing approximately 1.2 kb of the gene was exchanged with the respective sequence from the proviral clone. The wild-type gp120mn constructs used as controls were cloned by PCR from HIV-1 MN infected C8166 cells (AIDS Repository, Rockville, MD) and expressed gp120 either with a native envelope or a CD5 leader sequence. Since proviral clones were not available in this case, two clones of each construct were tested to avoid PCR artifacts. To determine the amount of secreted gp120 semi-quantitatively supernatants of 293T cells transiently transfected by calcium phosphate co-precipitation were immunoprecipitated with soluble CD4:immunoglobulin fusion protein and protein A sepharose.

The results of this analysis (Figure 3) show that the synthetic gene product is expressed at a very high level compared to that of the native gp120 controls. The molecular weight of the synthetic gp120 gene was comparable to control proteins (Figure 3) and appeared to be in the range of 100 to 110 kd. The slightly faster migration can be explained by the fact that in some tumor cell lines, e.g., 293T, glycosylation is either not complete or altered to some extent.

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To compare expression more accurately gp120 protein levels were quantitated using a gp120 ELISA with CD4 in the demobilized phase. This analysis shows (Figure 4) that ELISA data were comparable to the immunoprecipitation data, with a gp120 concentration of approximately 125 ng/ml for the synthetic gp120 gene, and less than the background cutoff (5 ng/ml) for all the native gp120 genes. Thus, expression of the synthetic gp120 gene appears to be at least one order of magnitude higher than wild-type gp120 genes. In the experiment shown the increase was at least 25 fold.

#### The Role of rev in gp120 Expression

Since rev appears to exert its effect at several steps in the expression of a viral transcript, the possible role of non-translational effects in the improved expression of the synthetic gp120 gene was tested. First, to rule out the possibility that negative signals elements conferring either increased mRNA degradation or nucleic retention were eliminated by changing the nucleotide sequence, cytoplasmic mRNA levels were tested. Cytoplasmic RNA was prepared by NP40 lysis of transiently transfected 293T cells and subsequent elimination of the nuclei by centrifugation. Cytoplasmic RNA was subsequently prepared from lysates by multiple phenol extractions and precipitation, spotted on nitrocellulose using a slot blot apparatus, and finally hybridized with an envelope-specific probe.

Briefly, cytoplasmic mRNA 293 cells transfected with CDM&, gp120 IIIB, or syngp120 was isolated 36 hours post transfection. Cytoplasmic RNA of Hela cells infected with wild-type vaccinia virus or recombinant virus expressing gp120 IIIB or the synthetic gp120 gene was under the control of the 7.5 promoter was isolated 16 hours post infection. Equal amounts were spotted on nitrocellulose using a slot

blot device and hybridized with randomly labeled 1.5 kb  
gp120IIIb and syngp120 fragments or human beta-actin. RNA  
expression levels were quantitated by scanning the  
hybridized membranes with a phosphorimager. The procedures  
5 used are described in greater detail below.

This experiment demonstrated that there was no  
significant difference in the mRNA levels of cells  
transfected with either the native or synthetic gp120 gene.  
In fact, in some experiments cytoplasmic mRNA level of the  
10 synthetic gp120 gene was even lower than that of the native  
gp120 gene.

These data were confirmed by measuring expression  
from recombinant vaccinia viruses. Human 293 cells or Hela  
cells were infected with vaccinia virus expressing wild-type  
15 gp120 IIIb or syngp120mn at a multiplicity of infection of  
at least 10. Supernatants were harvested 24 hours post  
infection and immunoprecipitated with CD4:immunoglobulin  
fusion protein and protein A sepharose. The procedures used  
in this experiment are described in greater detail below.

20 This experiment showed that the increased expression  
of the synthetic gene was still observed when the endogenous  
gene product and the synthetic gene product were expressed  
from vaccinia virus recombinants under the control of the  
strong mixed early and late 7.5k promoter. Because vaccinia  
25 virus mRNAs are transcribed and translated in the cytoplasm,  
increased expression of the synthetic envelope gene in this  
experiment cannot be attributed to improved export from the  
nucleus. This experiment was repeated in two additional  
human cell types, the kidney cancer cell line 293 and HeLa  
30 cells. As with transfected 293T cells, mRNA levels were  
similar in 293 cells infected with either recombinant  
vaccinia virus.

### Codon Usage in Lentivirus

Because it appears that codon usage has a significant impact on expression in mammalian cells, the codon frequency in the envelope genes of other retroviruses was examined. This study found no clear pattern of codon preference between retroviruses in general. However, if viruses from the lentivirus genus, to which HIV-1 belongs to, were analyzed separately, codon usage bias almost identical to that of HIV-1 was found. A codon frequency table from the envelope glycoproteins of a variety of (predominantly type C) retroviruses excluding the lentiviruses was prepared, and compared a codon frequency table created from the envelope sequences of four lentiviruses not closely related to HIV-1 (caprine arthritis encephalitis virus, equine infectious anemia virus, feline immunodeficiency virus, and visna virus) (Table 2). The codon usage pattern for lentiviruses is strikingly similar to that of HIV-1, in all cases but one, the preferred codon for HIV-1 is the same as the preferred codon for the other lentiviruses. The exception is proline, which is encoded by CCT in 41% of non-HIV lentiviral envelope residues, and by CCA in 40% of residues, a situation which clearly also reflects a significant preference for the triplet ending in A. The pattern of codon usage by the non-lentiviral envelope proteins does not show a similar predominance of A residues, and is also not as skewed toward third position C and G residues as is the codon usage for the highly expressed human genes. In general non-lentiviral retroviruses appear to exploit the different codons more equally, a pattern they share with less highly expressed human genes.

**TABLE 2:** Codon frequency in the envelope gene of lentiviruses (lenti) and non-lentiviral retroviruses (other)

			Other Lenti				Other Lenti	
5	<u>Ala</u>				<u>Cys</u>			
	GC	C	45	13	TG	C	53	21
		T	26	37		T	47	79
		A	20	46				
		G	9	3	<u>Gln</u>			
10	<u>Arg</u>				CA	A	52	69
	CG	C	14	2		G	48	31
		T	6	3	<u>Glu</u>			
		A	16	5	GA	A	57	68
15		G	17	3		G	43	32
	AG	A	31	51	<u>Gly</u>			
		G	15	26	GG	C	21	8
	<u>Asn</u>					T	13	9
20	AA	C	49	31		A	37	56
		T	51	69		G	29	26
	<u>Asp</u>				<u>His</u>			
	GA	C	55	33	CA	C	51	38
		T	51	69		T	49	62
25					<u>Ile</u>			
					AT	C	38	16
						T	31	22
						A	31	61
	<u>Leu</u>				<u>Ser</u>			
30	CT	C	22	8	TC	C	38	10
		T	14	9		T	17	16
		A	21	16		A	18	24
		G	19	11		G	6	5
	TT	A	15	41	AG	C	13	20
35		G	10	16		T	7	25
	<u>Lys</u>				<u>Thr</u>			
	AA	A	60	63	AC	C	44	18
		G	40	37		T	27	20
						A	19	55
						G	10	8
40	<u>Pro</u>				<u>Tyr</u>			
	CC	C	42	14	TA	C	48	28
		T	30	41		T	52	72
		A	20	40				
		G	7	5				

Phe

TT	C	52	25
	T	48	75

Val

GT	C	36	9
	T	17	10
	A	22	54
	G	25	27

5

Codon frequency was calculated using the GCG program established by the University of Wisconsin Genetics Computer Group. Numbers represent the percentage in which a particular codon is used. Codon usage of non-lentiviral retroviruses was compiled from the envelope precursor sequences of bovine leukemia virus feline leukemia virus, human T-cell leukemia virus type I, human T-cell lymphotropic virus type II, the mink cell focus-forming isolate of murine leukemia virus (MuLV), the Rauscher spleen focus-forming isolate, the 10A1 isolate, the 4070A amphotropic isolate and the myeloproliferative leukemia virus isolate, and from rat leukemia virus, simian sarcoma virus, simian T-cell leukemia virus, leukemogenic retrovirus T1223/B and gibbon ape leukemia virus. The codon frequency tables for the non-HIV, non-SIV lentiviruses were compiled from the envelope precursor sequences for caprine arthritis encephalitis virus, equine infectious anemia virus, feline immunodeficiency virus, and visna virus.

25

In addition to the prevalence of codons containing an A, lentiviral codons adhere to the HIV pattern of strong CpG under representation, so that the third position for alanine, proline, serine and threonine triplets is rarely G. The retroviral envelope triplets show a similar, but less pronounced, under representation of CpG. The most obvious difference between lentiviruses and other retroviruses with respect to CpG prevalence lies in the usage of the CGX variant of arginine triplets, which is reasonably frequently represented among the retroviral envelope coding sequences, but is almost never present among the comparable lentivirus sequences.

30

35

Differences in rev Dependence Between Native and Synthetic gp120

To examine whether regulation by rev is connected to HIV-1 codon usage, the influence of rev on the expression of both native and synthetic gene was investigated. Since regulation by rev requires the rev-binding site RRE in cis, constructs were made in which this binding site was cloned into the 3' untranslated region of both the native and the synthetic gene. These plasmids were co-transfected with rev or a control plasmid in trans into 293T cells, and gp120 expression levels in supernatants were measured semiquantitatively by immunoprecipitation. The procedures used in this experiment are described in greater detail below.

As shown in Figure 5A and Figure 5B, rev up regulates the native gp120 gene, but has no effect on the expression of the synthetic gp120 gene. Thus, the action of rev is not apparent on a substrate which lacks the coding sequence of endogenous viral envelope sequences.

Expression of a synthetic ratTHY-1 gene with HIV envelope codons

The above-described experiment suggest that in fact "envelope sequences" have to be present for rev regulation. In order to test this hypothesis, a synthetic version of the gene encoding the small, typically highly expressed cell surface protein, ratTHY-1 antigen, was prepared. The synthetic version of the ratTHY-1 gene was designed to have a codon usage like that of HIV gp120. In designing this synthetic gene AUUUA sequences, which are associated with mRNA instability, were avoided. In addition, two restriction sites were introduced to simplify manipulation of the resulting gene (Figure 6). This synthetic gene with the HIV envelope codon usage (rTHY-1env) was generated using

three 150 to 170 mer oligonucleotides (Figure 7). In contrast to the syngp120mn gene, PCR products were directly cloned and assembled in pUC12, and subsequently cloned into pCDM7.

5           Expression levels of native rTHY-1 and rTHY-1 with the HIV envelope codons were quantitated by immunofluorescence of transiently transfected 293T cells. Figure 8 shows that the expression of the native THY-1 gene is almost two orders of magnitude above the background level  
10 of the control transfected cells (pCDM7). In contrast, expression of the synthetic ratTHY-1 is substantially lower than that of the native gene (shown by the shift to of the peak towards a lower channel number).

To prove that no negative sequence elements  
15 promoting mRNA degradation were inadvertently introduced, a construct was generated in which the rTHY-1env gene was cloned at the 3' end of the synthetic gp120 gene (Figure 9B). In this experiment 293T cells were transfected with either the syngp120mn gene or the syngp120/ratTHY-1 env  
20 fusion gene (syngp120mn.rTHY-1env). Expression was measured by immunoprecipitation with CD4:IgG fusion protein and protein A agarose. The procedures used in this experiment are described in greater detail below.

Since the synthetic gp120 gene has an UAG stop  
25 codon, rTHY-1env is not translated from this transcript. If negative elements conferring enhanced degradation were present in the sequence, gp120 protein levels expressed from this construct should be decreased in comparison to the syngp120mn construct without rTHY-1env. Figure 9A, shows  
30 that the expression of both constructs is similar, indicating that the low expression must be linked to translation.

Rev-dependent expression of synthetic ratTHY-1 gene  
with envelope codons

To explore whether rev is able to regulate expression of a ratTHY-1 gene having env codons, a construct was made with a rev-binding site in the 3' end of the rTHY1env open reading frame. To measure rev-responsiveness of the a ratTHY-1env construct having a 3' RRE, human 293T cells were cotransfected ratTHY-1envrre and either CDM7 or pCMVrev. At 60 hours post transfection cells were detached with 1 mM EDTA in PBS and stained with the OX-7 anti rTHY-1 mouse monoclonal antibody and a secondary FITC-conjugated antibody. Fluorescence intensity was measured using a EPICS XL cytofluorometer. These procedures are described in greater detail below.

In repeated experiments, a slight increase of rTHY-1env expression was detected if rev was cotransfected with the rTHY-1env gene. To further increase the sensitivity of the assay system a construct expressing a secreted version of rTHY-1env was generated. This construct should produce more reliable data because the accumulated amount of secreted protein in the supernatant reflects the result of protein production over an extended period, in contrast to surface expressed protein, which appears to more closely reflect the current production rate. A gene capable of expressing a secreted form was prepared by PCR using forward and reverse primers annealing 3' of the endogenous leader sequence and 5' of the sequence motif required for phosphatidylinositol glycan anchorage respectively. The PCR product was cloned into a plasmid which already contained a CD5 leader sequence, thus generating a construct in which the membrane anchor has been deleted and the leader sequence exchanged by a heterologous (and probably more efficient) leader peptide.

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The rev-responsiveness of the secreted form ratTHY-1env was measured by immunoprecipitation of supernatants of human 293T cells cotransfected with a plasmid expressing a secreted form of ratTHY-1env and the RRE sequence in cis (rTHY-1envPI-rre) and either CDM7 or pCMVrev. The rTHY-1envPI-RRE construct was made by PCR using the oligonucleotide: cgcggggctagcgcaaagagtaataagtttaac (SEQ ID NO:38) as a forward primer, the oligonucleotide: cgcggatcccttgatattttgtactaata (SEQ ID NO:39) as reverse primer, and the synthetic rTHY-1env construct as a template. After digestion with Nhe1 and Not1 the PCR fragment was cloned into a plasmid containing CD5 leader and RRE sequences. Supernatants of <sup>35</sup>S labeled cells were harvested 72 hours post transfection, precipitated with a mouse monoclonal antibody OX7 against rTHY-1 and anti mouse IgG sepharose, and run on a 12% reducing SDS-PAGE.

In this experiment the induction of rTHY-1env by rev was much more prominent and clear-cut than in the above-described experiment and strongly suggests that rev is able to translationally regulate transcripts that are suppressed by low-usage codons.

Rev-independent expression of a rTHY-1env:immunoglobulin fusion protein

To test whether low-usage codons must be present throughout the whole coding sequence or whether a short region is sufficient to confer rev-responsiveness, a rTHY-1env:immunoglobulin fusion protein was generated. In this construct the rTHY-1env gene (without the sequence motif responsible for phosphatidylinositol glycan anchorage) is linked to the human IgG1 hinge, CH2 and CH3 domains. This construct was generated by anchor PCR using primers with Nhe1 and BamHI restriction sites and rTHY-1env as template. The PCR fragment was cloned into a plasmid

containing the leader sequence of the CD5 surface molecule and the hinge, CH2 and CH3 parts of human IgG1 immunoglobulin. A Hind3/Eag1 fragment containing the rTHY-1envgl insert was subsequently cloned into a pCDM7-  
5 derived plasmid with the RRE sequence.

To measure the response of the rTHY-1env/  
immunoglobulin fusion gene (rTHY-1envglrre) to rev human 293T cells cotransfected with rTHY-1envglrre and either pCDM7 or pCMVrev. The rTHY-1envglrre construct was made by anchor  
10 PCR using forward and reverse primers with Nhe1 and BamH1 restriction sites respectively. The PCR fragment was cloned into a plasmid containing a CD5 leader and human IgG1 hinge, CH2 and CH3 domains. Supernatants of <sup>35</sup>S labeled cells were harvested 72 hours post transfection,  
15 precipitated with a mouse monoclonal antibody OX7 against rTHY-1 and anti mouse IgG sepharose, and run on a 12% reducing SDS-PAGE. The procedures used are described in greater detail below.

As with the product of the rTHY-1envPI- gene, this  
20 rTHY-1env/immunoglobulin fusion protein is secreted into the supernatant. Thus, this gene should be responsive to rev-induction. However, in contrast to rTHY-1envPI-, cotransfection of rev in trans induced no or only a negligible increase of rTHY-1envgl expression.

25 The expression of rTHY-1:immunoglobulin fusion protein with native rTHY-1 or HIV envelope codons was measured by immunoprecipitation. Briefly, human 293T cells transfected with either rTHY-1envgl (env codons) or rTHY-1wtegl (native codons). The rTHY-1wtegl construct was  
30 generated in manner similar to that used for the rTHY-1envgl construct, with the exception that a plasmid containing the native rTHY-1 gene was used as template. Supernatants of <sup>35</sup>S labeled cells were harvested 72 hours

post transfection, precipitated with a mouse monoclonal antibody OX7 against rTHY-1 and anti mouse IgG sepharose, and run on a 12% reducing SDS-PAGE. THE procedures used in this experiment are described in greater detail below.

5           Expression levels of rTHY-1env<sub>g1</sub> were decreased in comparison to a similar construct with wild-type rTHY-1 as the fusion partner, but were still considerably higher than rTHY-1env. Accordingly, both parts of the fusion protein influenced expression levels. The addition of rTHY-1env did  
10 not restrict expression to an equal level as seen for rTHY-1env alone. Thus, regulation by rev appears to be ineffective if protein expression is not almost completely suppressed.

#### Codon preference in HIV-1 envelope genes

15           Direct comparison between codon usage frequency of HIV envelope and highly expressed human genes reveals a striking difference for all twenty amino acids. One simple measure of the statistical significance of this codon preference is the finding that among the nine amino acids  
20 with two fold codon degeneracy, the favored third residue is A or U in all nine. The probability that all nine of two equiprobable choices will be the same is approximately 0.004, and hence by any conventional measure the third residue choice cannot be considered random. Further  
25 evidence of a skewed codon preference is found among the more degenerate codons, where a strong selection for triplets bearing adenine can be seen. This contrasts with the pattern for highly expressed genes, which favor codons bearing C, or less commonly G, in the third position of  
30 codons with three or more fold degeneracy.

          The systematic exchange of native codons with codons of highly expressed human genes dramatically increased expression of gp120. A quantitative analysis by ELISA

showed that expression of the synthetic gene was at least 25 fold higher in comparison to native gp120 after transient transfection into human 293 cells. The concentration levels in the ELISA experiment shown were rather low. Since an  
5 ELISA was used for quantification which is based on gp120 binding to CD4, only native, non-denatured material was detected. This may explain the apparent low expression. Measurement of cytoplasmic mRNA levels demonstrated that the difference in protein expression is due to translational  
10 differences and not mRNA stability.

Retroviruses in general do not show a similar preference towards A and T as found for HIV. But if this family was divided into two subgroups, lentiviruses and non-lentiviral retroviruses, a similar preference to A and, less  
15 frequently, T, was detected at the third codon position for lentiviruses. Thus, the availing evidence suggests that lentiviruses retain a characteristic pattern of envelope codons not because of an inherent advantage to the reverse transcription or replication of such residues, but rather  
20 for some reason peculiar to the physiology of that class of viruses. The major difference between lentiviruses and non-complex retroviruses are additional regulatory and non-essentially accessory genes in lentiviruses, as already mentioned. Thus, one simple explanation for the restriction  
25 of envelope expression might be that an important regulatory mechanism of one of these additional molecules is based on it. In fact, it is known that one of these proteins, rev, which most likely has homologues in all lentiviruses. Thus codon usage in viral mRNA is used to create a class of  
30 transcripts which is susceptible to the stimulatory action of rev. This hypothesis was proved using a similar strategy as above, but this time codon usage was changed into the inverse direction. Codon usage of a highly expressed

cellular gene was substituted with the most frequently used codons in the HIV envelope. As assumed, expression levels were considerably lower in comparison to the native molecule, almost two orders of magnitude when analyzed by immunofluorescence of the surface expressed molecule. If rev was coexpressed in trans and a RRE element was present in cis only a slight induction was found for the surface molecule. However, if THY-1 was expressed as a secreted molecule, the induction by rev was much more prominent, supporting the above hypothesis. This can probably be explained by accumulation of secreted protein in the supernatant, which considerably amplifies the rev effect. If rev only induces a minor increase for surface molecules in general, induction of HIV envelope by rev cannot have the purpose of an increased surface abundance, but rather of an increased intracellular gp160 level. It is completely unclear at the moment why this should be the case.

To test whether small subtotal elements of a gene are sufficient to restrict expression and render it rev-dependent rTHY1env:immunoglobulin fusion proteins were generated, in which only about one third of the total gene had the envelope codon usage. Expression levels of this construct were on an intermediate level, indicating that the rTHY-1env negative sequence element is not dominant over the immunoglobulin part. This fusion protein was not or only slightly rev-responsive, indicating that only genes almost completely suppressed can be rev-responsive.

Another characteristic feature that was found in the codon frequency tables is a striking under representation of CpG triplets. In a comparative study of codon usage in E. coli, yeast, drosophila and primates it was shown that in a high number of analyzed primate genes the 8 least used codons contain all codons with the CpG dinucleotide

sequence. Avoidance of codons containing this dinucleotide motif was also found in the sequence of other retroviruses. It seems plausible that the reason for under representation of CpG-bearing triplets has something to do with avoidance of gene silencing by methylation of CpG cytosines. The expected number of CpG dinucleotides for HIV as a whole is about one fifth that expected on the basis of the base composition. This might indicate that the possibility of high expression is restored, and that the gene in fact has to be highly expressed at some point during viral pathogenesis.

The results presented herein clearly indicate that codon preference has a severe effect on protein levels, and suggest that translational elongation is controlling mammalian gene expression. However, other factors may play a role. First, abundance of not maximally loaded mRNA's in eukaryotic cells indicates that initiation is rate limiting for translation in at least some cases, since otherwise all transcripts would be completely covered by ribosomes. Furthermore, if ribosome stalling and subsequent mRNA degradation were the mechanism, suppression by rare codons could most likely not be reversed by any regulatory mechanism like the one presented herein. One possible explanation for the influence of both initiation and elongation on translational activity is that the rate of initiation, or access to ribosomes, is controlled in part by cues distributed throughout the RNA, such that the lentiviral codons predispose the RNA to accumulate in a pool of poorly initiated RNAs. However, this limitation need not be kinetic; for example, the choice of codons could influence the probability that a given translation product, once initiated, is properly completed. Under this mechanism, abundance of less favored codons would incur a

significant cumulative probability of failure to complete the nascent polypeptide chain. The sequestered RNA would then be lent an improved rate of initiation by the action of rev. Since adenine residues are abundant in rev-responsive transcripts, it could be that RNA adenine methylation

#### Detailed Procedures

The following procedures were used in the above-described experiments.

#### Sequence Analysis

Sequence analyses employed the software developed by the University of Wisconsin Computer Group.

#### Plasmid constructions

Plasmid constructions employed the following methods. Vectors and insert DNA was digested at a concentration of 0.5  $\mu\text{g}/10\ \mu\text{l}$  in the appropriate restriction buffer for 1 - 4 hours (total reaction volume approximately 30  $\mu\text{l}$ ). Digested vector was treated with 10% (v/v) of 1  $\mu\text{g}/\text{ml}$  calf intestine alkaline phosphatase for 30 min prior to gel electrophoresis. Both vector and insert digests (5 to 10  $\mu\text{l}$  each) were run on a 1.5% low melting agarose gel with TAE buffer. Gel slices containing bands of interest were transferred into a 1.5 ml reaction tube, melted at 65°C and directly added to the ligation without removal of the agarose. Ligations were typically done in a total volume of 25  $\mu\text{l}$  in 1x Low Buffer 1x Ligation Additions with 200-400 U of ligase, 1  $\mu\text{l}$  of vector, and 4  $\mu\text{l}$  of insert. When necessary, 5' overhanging ends were filled by adding 1/10 volume of 250  $\mu\text{M}$  dNTPs and 2-5 U of Klenow polymerase to heat inactivated or phenol extracted digests and incubating for approximately 20 min at room temperature. When necessary, 3' overhanging ends were filled by adding 1/10 volume of 2.5 mM dNTPs and 5-10 U of T4 DNA polymerase to

heat inactivated or phenol extracted digests, followed by incubation at 37°C for 30 min. The following buffers were used in these reactions: 10x Low buffer (60 mM Tris HCl, pH 7.5, 60 mM MgCl<sub>2</sub>, 50 mM NaCl, 4 mg/ml BSA, 70 mM β-

5 mercaptoethanol, 0.02% NaN<sub>3</sub>); 10x Medium buffer (60 mM Tris HCl, pH 7.5, 60 mM MgCl<sub>2</sub>, 50 mM NaCl, 4 mg/ml BSA, 70 mM β-mercaptoethanol, 0.02% NaN<sub>3</sub>); 10x High buffer (60 mM Tris HCl, pH 7.5, 60 mM MgCl<sub>2</sub>, 50 mM NaCl, 4 mg/ml BSA, 70 mM β-mercaptoethanol, 0.02% NaN<sub>3</sub>); 10x Ligation additions (1 mM  
10 ATP, 20 mM DTT, 1 mg/ml BSA, 10 mM spermidine); 50x TAE (2 M Tris acetate, 50 mM EDTA).

#### Oligonucleotide synthesis and purification

Oligonucleotides were produced on a Milligen 8750 synthesizer (Millipore). The columns were eluted with 1 ml  
15 of 30% ammonium hydroxide, and the eluted oligonucleotides were deblocked at 55°C for 6 to 12 hours. After deblocking, 150 μl of oligonucleotide were precipitated with 10x volume of unsaturated n-butanol in 1.5 ml reaction tubes, followed by centrifugation at 15,000 rpm in a  
20 microfuge. The pellet was washed with 70% ethanol and resuspended in 50 μl of H<sub>2</sub>O. The concentration was determined by measuring the optical density at 260 nm in a dilution of 1:333 (1 OD<sub>260</sub> = 30 μg/ml).

The following oligonucleotides were used for  
25 construction of the synthetic gp120 gene (all sequences shown in this text are in 5' to 3' direction).

oligo 1 forward (Nhe1): cgc ggg cta gcc acc gag aag  
ctg (SEQ ID NO:1).

oligo 1: acc gag aag ctg tgg gtg acc gtg tac tac  
30 ggc gtg ccc gtg tgg aag ag ag gcc acc acc acc ctg ttc tgc  
gcc agc gac gcc aag gcg tac gac acc gag gtg cac aac gtg tgg  
gcc acc cag gcg tgc gtg ccc acc gac ccc aac ccc cag gag gtg  
gag ctc gtg aac gtg acc gag aac ttc aac at (SEQ ID NO:2).

oligo 1 reverse: cca cca tgt tgt tct tcc aca tgt tga  
agt tct c (SEQ ID NO:3).

oligo 2 forward: gac cga gaa ctt caa cat gtg gaa  
gaa caa cat (SEQ ID NO:4)

5 oligo 2: tgg aag aac aac atg gtg gag cag atg cat gag  
gac atc atc agc ctg tgg gac cag agc ctg aag ccc tgc gtg aag  
ctg acc cc ctg tgc gtg acc tg aac tgc acc gac ctg agg aac  
acc acc aac acc aac ac agc acc gcc aac aac aac agc aac agc  
gag ggc acc atc aag ggc ggc gag atg (SEQ ID NO:5).

10 oligo 2 reverse (Pst1): gtt gaa gct gca gtt ctt cat  
ctc gcc gcc ctt (SEQ ID NO:6).

oligo 3 forward (Pst1): gaa gaa ctg cag ctt caa cat  
cac cac cag c (SEQ ID NO:7).

15 oligo 3: aac atc acc acc agc atc cgc gac aag atg cag  
aag gag tac gcc ctg ctg tac aag ctg gat atc gtg agc atc gac  
aac gac agc acc agc tac cgc ctg atc tcc tgc aac acc agc gtg  
atc acc cag gcc tgc ccc aag atc agc ttc gag ccc atc ccc atc  
cac tac tgc gcc ccc gcc ggc ttc gcc (SEQ ID NO:8).

20 oligo 3 reverse: gaa ctt ctt gtc ggc ggc gaa gcc  
ggc ggc (SEQ ID NO:9).

oligo 4 forward: gcg ccc ccg ccg gct tcg cca tcc  
tga agt gca acg aca aga agt tc (SEQ ID NO:10)

25 oligo 4: gcc gac aag aag ttc agc ggc aag ggc agc  
tgc aag aac gtg agc acc gtg cag tgc acc cac ggc atc ccg ccg  
gtg gtg agc acc cag ctc ctg ctg aac ggc agc ctg gcc gag gag  
gag gtg gtg atc cgc agc gag aac ttc acc gac aac gcc aag acc  
atc atc gtg cac ctg aat gag agc gtg cag atc (SEQ ID NO:11)

oligo 4 reverse (Mlu1): agt tgg gac gcg tgc agt tga  
tct gca cgc tct c (SEQ ID NO:12).

30 oligo 5 forward (Mlu1): gag agc gtg cag atc aac tgc  
acg cgt ccc (SEQ ID NO:13).

oligo 5: aac tgc acg cgt ccc aac tac aac aag cgc  
aag cgc atc cac atc ggc ccc ggc cgc gcc ttc tac acc acc aag

aac atc atc ggc acc atc ctc cag gcc cac tgc aac atc tct aga  
(SEQ ID NO:14) .

oligo 5 reverse: gtc gtt cca ctt ggc tct aga gat  
gtt gca (SEQ ID NO:15).

5 oligo 6 forward: gca aca tct cta gag cca agt gga  
acg ac (SEQ ID NO:16).

oligo 6: gcc aag tgg aac gac acc ctg cgc cag atc  
gtg agc aag ctg aag gag cag ttc aag aac aag acc atc gtg ttc  
ac cag agc agc ggc ggc gac ccc gag atc gtg atg cac agc ttc  
10 aac tgc ggc ggc (SEQ ID NO:17).

oligo 6 reverse (EcoR1): gca gta gaa gaa ttc gcc gcc  
gca gtt ga (SEQ ID NO:18).

oligo 7 forward (EcoR1): tca act gcg gcg gcg aat  
tct tct act gc (SEQ ID NO:19).

15 oligo 7: ggc gaa ttc ttc tac tgc aac acc agc ccc  
ctg ttc aac agc acc tgg aac ggc aac aac acc tgg aac aac acc  
acc ggc agc aac aac aat att acc ctc cag tgc aag atc aag cag  
atc atc aac atg tgg cag gag gtg ggc aag gcc atg tac gcc ccc  
ccc atc gag ggc cag atc cgg tgc agc agc (SEQ ID NO:20)

20 oligo 7 reverse: gca gac cgg tga tgt tgc tgc tgc  
acc gga tct ggc cct c (SEQ ID NO:21).

oligo 8 forward: cga ggg cca gat ccg gtg cag cag  
caa cat cac cgg tct g (SEQ ID NO:22).

oligo 8: aac atc acc ggt ctg ctg ctg acc cgc gac  
25 ggc ggc aag gac acc gac acc aac gac acc gaa atc ttc cgc ccc  
ggc ggc ggc gac atg cgc gac aac tgg aga tct gag ctg tac aag  
tac aag gtg gtg acg atc gag ccc ctg ggc gtg gcc ccc acc aag  
gcc aag cgc cgc gtg gtg cag cgc gag aag cgc (SEQ ID NO:23).

oligo 8 reverse (NotI): cgc ggg cgg ccg ctt tag cgc  
30 ttc tcg cgc tgc acc ac (SEQ ID NO:24).

The following oligonucleotides were used for the  
construction of the ratTHY-1env gene.

oligo 1 forward (BamH1/Hind3): cgc ggg gga tcc aag  
ctt acc atg att cca gta ata agt (SEQ ID NO:25).

oligo 1: atg aat cca gta ata agt ata aca tta tta  
tta agt gta tta caa atg agt aga gga caa aga gta ata agt tta  
5 aca gca tct tta gta aat caa aat ttg aga tta gat tgt aga cat  
gaa aat aat aca aat ttg cca ata caa cat gaa ttt tca tta acg  
(SEQ ID NO:26).

oligo 1 reverse (EcoR1/Mlu1): cgc ggg gaa ttc acg  
cgt taa tga aaa ttc atg ttg (SEQ ID NO:27).

10 oligo 2 forward (BamH1/Mlu1): cgc gga tcc acg cgt  
gaa aaa aaa aaa cat (SEQ ID NO:28).

oligo 2: cgt gaa aaa aaa aaa cat gta tta agt gga  
aca tta gga gta cca gaa cat aca tat aga agt aga gta aat ttg  
ttt agt gat aga ttc ata aaa gta tta aca tta gca aat ttt aca  
15 aca aaa gat gaa gga gat tat atg tgt gag (SEQ ID NO:29).

oligo 2 reverse (EcoR1/Sac1): cgc gaa ttc gag ctc  
aca cat ata atc tcc (SEQ ID NO:30).

oligo 3 forward (BamH1/Sac1): cgc gga tcc gag ctc  
aga gta agt gga caa (SEQ ID NO:31).

20 oligo 3: ctc aga gta agt gga caa aat cca aca agt  
agt aat aaa aca ata aat gta ata aga gat aaa tta gta aaa tgt  
ga gga ata agt tta tta gta caa aat aca agt tgg tta tta tta  
tta tta tta agt tta agt ttt tta caa gca aca gat ttt ata agt  
tta tga (SEQ ID NO:32).

25 oligo 3 reverse (EcoR1/Not1): cgc gaa ttc gcg gcc  
gct tca taa act tat aaa atc (SEQ ID NO:33).

#### Polymerase Chain Reaction

Short, overlapping 15 to 25 mer oligonucleotides  
annealing at both ends were used to amplify the long  
30 oligonucleotides by polymerase chain reaction (PCR). Typical  
PCR conditions were: 35 cycles, 55°C annealing temperature,  
0.2 sec extension time. PCR products were gel purified,  
phenol extracted, and used in a subsequent PCR to generate

longer fragments consisting of two adjacent small fragments. These longer fragments were cloned into a CDM7-derived plasmid containing a leader sequence of the CD5 surface molecule followed by a Nhe1/Pst1/Mlu1/EcoR1/BamH1 polylinker.

The following solutions were used in these reactions: 10x PCR buffer (500 mM KCl, 100 mM Tris HCl, pH 7.5, 8 mM MgCl<sub>2</sub>, 2 mM each dNTP). The final buffer was complemented with 10% DMSO to increase fidelity of the Taq polymerase.

#### Small scale DNA preparation

Transformed bacteria were grown in 3 ml LB cultures for more than 6 hours or overnight. Approximately 1.5 ml of each culture was poured into 1.5 ml microfuge tubes, spun for 20 seconds to pellet cells and resuspended in 200  $\mu$ l of solution I. Subsequently 400  $\mu$ l of solution II and 300  $\mu$ l of solution III were added. The microfuge tubes were capped, mixed and spun for > 30 sec. Supernatants were transferred into fresh tubes and phenol extracted once. DNA was precipitated by filling the tubes with isopropanol, mixing, and spinning in a microfuge for > 2 min. The pellets were rinsed in 70 % ethanol and resuspended in 50  $\mu$ l dH<sub>2</sub>O containing 10  $\mu$ l of RNase A. The following media and solutions were used in these procedures: LB medium (1.0 % NaCl, 0.5% yeast extract, 1.0% trypton); solution I (10 mM EDTA pH 8.0); solution II (0.2 M NaOH, 1.0% SDS); solution III (2.5 M KOAc, 2.5 M glacial acetic acid); phenol (pH adjusted to 6.0, overlaid with TE); TE (10 mM Tris HCl, pH 7.5, 1 mM EDTA pH 8.0).

#### Large scale DNA preparation

One liter cultures of transformed bacteria were grown 24 to 36 hours (MC1061p3 transformed with pCDM derivatives) or 12 to 16 hours (MC1061 transformed with pUC

derivatives) at 37°C in either M9 bacterial medium (pCDM derivatives) or LB (pUC derivatives). Bacteria were spun down in 1 liter bottles using a Beckman J6 centrifuge at 4,200 rpm for 20 min. The pellet was resuspended in 40 ml of solution I. Subsequently, 80 ml of solution II and 40 ml of solution III were added and the bottles were shaken semivigorously until lumps of 2 to 3 mm size developed. The bottle was spun at 4,200 rpm for 5 min and the supernatant was poured through cheesecloth into a 250 ml bottle.

Isopropanol was added to the top and the bottle was spun at 4,200 rpm for 10 min. The pellet was resuspended in 4.1 ml of solution I and added to 4.5 g of cesium chloride, 0.3 ml of 10 mg/ml ethidium bromide, and 0.1 ml of 1% Triton X100 solution. The tubes were spun in a Beckman J2 high speed centrifuge at 10,000 rpm for 5 min. The supernatant was transferred into Beckman Quick Seal ultracentrifuge tubes, which were then sealed and spun in a Beckman ultracentrifuge using a NVT90 fixed angle rotor at 80,000 rpm for > 2.5 hours. The band was extracted by visible light using a 1 ml syringe and 20 gauge needle. An equal volume of dH<sub>2</sub>O was added to the extracted material. DNA was extracted once with n-butanol saturated with 1 M sodium chloride, followed by addition of an equal volume of 10 M ammonium acetate/ 1 mM EDTA. The material was poured into a 13 ml snap tube which was then filled to the top with absolute ethanol, mixed, and spun in a Beckman J2 centrifuge at 10,000 rpm for 10 min. The pellet was rinsed with 70% ethanol and resuspended in 0.5 to 1 ml of H<sub>2</sub>O. The DNA concentration was determined by measuring the optical density at 260 nm in a dilution of 1:200 (1 OD<sub>260</sub> = 50 µg/ml).

The following media and buffers were used in these procedures: M9 bacterial medium (10 g M9 salts, 10 g

casamino acids (hydrolyzed), 10 ml M9 additions, 7.5  $\mu\text{g/ml}$  tetracycline (500  $\mu\text{l}$  of a 15 mg/ml stock solution), 12.5  $\mu\text{g/ml}$  ampicillin (125  $\mu\text{l}$  of a 10 mg/ml stock solution); M9 additions (10 mM  $\text{CaCl}_2$ , 100 mM  $\text{MgSO}_4$ , 200  $\mu\text{g/ml}$  thiamine, 5 70% glycerol); LB medium (1.0 % NaCl, 0.5 % yeast extract, 1.0 % trypton); Solution I (10 mM EDTA pH 8.0); Solution II (0.2 M NaOH 1.0 % SDS); Solution III (2.5 M KOAc 2.5 M HOAc)

#### Sequencing

Synthetic genes were sequenced by the Sanger  
10 dideoxynucleotide method. In brief, 20 to 50  $\mu\text{g}$  double-stranded plasmid DNA were denatured in 0.5 M NaOH for 5 min. Subsequently the DNA was precipitated with 1/10 volume of sodium acetate (pH 5.2) and 2 volumes of ethanol and centrifuged for 5 min. The pellet was washed with 70%  
15 ethanol and resuspended at a concentration of 1  $\mu\text{g}/\mu\text{l}$ . The annealing reaction was carried out with 4  $\mu\text{g}$  of template DNA and 40 ng of primer in 1x annealing buffer in a final volume of 10  $\mu\text{l}$ . The reaction was heated to 65°C and slowly cooled to 37°C.

20 In a separate tube 1  $\mu\text{l}$  of 0.1 M DTT, 2  $\mu\text{l}$  of labeling mix, 0.75  $\mu\text{l}$  of  $\text{dH}_2\text{O}$ , 1  $\mu\text{l}$  of [ $^{35}\text{S}$ ] dATP (10  $\mu\text{Ci}$ ), and 0.25  $\mu\text{l}$  of Sequenase™ (12 U/ $\mu\text{l}$ ) were added for each reaction. Five  $\mu\text{l}$  of this mix were added to each annealed primer-template tube and incubated for 5 min at room  
25 temperature. For each labeling reaction 2.5  $\mu\text{l}$  of each of the 4 termination mixes were added on a Terasaki plate and prewarmed at 37°C. At the end of the incubation period 3.5  $\mu\text{l}$  of labeling reaction were added to each of the 4 termination mixes. After 5 min, 4  $\mu\text{l}$  of stop solution were  
30 added to each reaction and the Terasaki plate was incubated at 80°C for 10 min in an oven. The sequencing reactions were run on 5% denaturing polyacrylamide gel. An acrylamide solution was prepared by adding 200 ml of 10x TBE buffer and

957 ml of dH<sub>2</sub>O to 100 g of acrylamide:bisacrylamide (29:1).  
5% polyacrylamide 46% urea and 1x TBE gel was prepared by  
combining 38 ml of acrylamide solution and 28 g urea.  
Polymerization was initiated by the addition of 400  $\mu$ l of  
5 10% ammonium peroxodisulfate and 60  $\mu$ l of TEMED. Gels were  
poured using silanized glass plates and sharktooth combs and  
run in 1x TBE buffer at 60 to 100 W for 2 to 4 hours  
(depending on the region to be read). Gels were transferred  
to Whatman blotting paper, dried at 80°C for about 1 hour,  
10 and exposed to x-ray film at room temperature. Typically  
exposure time was 12 hours. The following solutions were  
used in these procedures: 5x Annealing buffer (200 mM Tris  
HCl, pH 7.5, 100 mM MgCl<sub>2</sub>, 250 mM NaCl); Labelling Mix (7.5  
 $\mu$ M each dCTP, dGTP, and dTTP); Termination Mixes (80  $\mu$ M each  
15 dNTP, 50 mM NaCl, 8  $\mu$ M ddNTP (one each)); Stop solution (95%  
formamide, 20 mM EDTA, 0.05 % bromphenol blue, 0.05 %  
xylencyanol); 5x TBE (0.9 M Tris borate, 20 mM EDTA);  
Polyacrylamide solution (96.7 g polyacrylamide, 3.3 g  
bisacrylamide, 200 ml 1x TBE, 957 ml dH<sub>2</sub>O).

#### 20 RNA isolation

Cytoplasmic RNA was isolated from calcium phosphate  
transfected 293T cells 36 hours post transfection and from  
vaccinia infected Hela cells 16 hours post infection  
essentially as described by Gilman. (Gilman Preparation of  
25 cytoplasmic RNA from tissue culture cells. In Current  
Protocols in Molecular Biology, Ausubel et al., eds., Wiley  
& Sons, New York, 1992). Briefly, cells were lysed in 400  
 $\mu$ l lysis buffer, nuclei were spun out, and SDS and  
proteinase K were added to 0.2% and 0.2 mg/ml respectively.  
30 The cytoplasmic extracts were incubated at 37°C for 20 min,  
phenol/chloroform extracted twice, and precipitated. The  
RNA was dissolved in 100  $\mu$ l buffer I and incubated at 37°C

for 20 min. The reaction was stopped by adding 25  $\mu$ l stop buffer and precipitated again.

The following solutions were used in this procedure:  
Lysis Buffer (TRUSTEE containing with 50 mM Tris pH 8.0, 100  
5 mM NaCl, 5 mM MgCl<sub>2</sub>, 0.5% NP40); Buffer I (TRUSTEE buffer  
with 10 mM MgCl<sub>2</sub>, 1 mM DTT, 0.5 U/ $\mu$ l placental RNase  
inhibitor, 0.1 U/ $\mu$ l RNase free DNase I); Stop buffer (50 mM  
EDTA 1.5 M NaOAc 1.0% SDS).

#### Slot blot analysis

10 For slot blot analysis 10  $\mu$ g of cytoplasmic RNA was  
dissolved in 50  $\mu$ l dH<sub>2</sub>O to which 150  $\mu$ l of 10x SSC/18%  
formaldehyde were added. The solubilized RNA was then  
incubated at 65°C for 15 min and spotted onto with a slot  
blot apparatus. Radioactively labeled probes of 1.5 kb  
15 gp120IIIb and syngp120mn fragments were used for  
hybridization. Each of the two fragments was random labeled  
in a 50  $\mu$ l reaction with 10  $\mu$ l of 5x oligo-labeling buffer,  
8  $\mu$ l of 2.5 mg/ml BSA, 4  $\mu$ l of [ $\alpha$ <sup>32</sup>P]-dCTP (20 uCi/ $\mu$ l; 6000  
Ci/mmol), and 5 U of Klenow fragment. After 1 to 3 hours  
20 incubation at 37°C 100  $\mu$ l of TRUSTEE were added and  
unincorporated [ $\alpha$ <sup>32</sup>P]-dCTP was eliminated using G50 spin  
column. Activity was measured in a Beckman beta-counter,  
and equal specific activities were used for hybridization.  
Membranes were pre-hybridized for 2 hours and hybridized for  
25 12 to 24 hours at 42°C with 0.5 x 10<sup>6</sup> cpm probe per ml  
hybridization fluid. The membrane was washed twice (5 min)  
with washing buffer I at room temperature, for one hour in  
washing buffer II at 65°C, and then exposed to x-ray film.  
Similar results were obtained using a 1.1 kb Not1/Sfi1  
30 fragment of pCDM7 containing the 3 untranslated region.  
Control hybridizations were done in parallel with a random-  
labeled human beta-actin probe. RNA expression was

quantitated by scanning the hybridized nitrocellulose membranes with a Magnetic Dynamics phosphorimager.

The following solutions were used in this procedure:

5x Oligo-labeling buffer (250 mM Tris HCl, pH 8.0, 25 mM  
5 MgCl<sub>2</sub>, 5 mM β-mercaptoethanol, 2 mM dATP, 2 mM dGTP, mM  
dTTP, 1 M Hepes pH 6.6, 1 mg/ml hexanucleotides [dNTP]6);  
Hybridization Solution (.05 M sodium phosphate, 250 mM NaCl,  
7% SDS, 1 mM EDTA, 5% dextrane sulfate, 50% formamide, 100  
μg/ml denatured salmon sperm DNA); Washing buffer I (2x SSC,  
10 0.1% SDS); Washing buffer II (0.5x SSC, 0.1 % SDS); 20x SSC  
(3 M NaCl, 0.3 M Na<sub>3</sub>citrate, pH adjusted to 7.0).

#### Vaccinia recombination

Vaccinia recombination used a modification of the of  
the method described by Romeo and Seed (Romeo and Seed,  
15 Cell, 64: 1037, 1991). Briefly, CV1 cells at 70 to 90%  
confluency were infected with 1 to 3 μl of a wild-type  
vaccinia stock WR (2 x 10<sup>8</sup> pfu/ml) for 1 hour in culture  
medium without calf serum. After 24 hours, the cells were  
transfected by calcium phosphate with 25 μg TKG plasmid DNA  
20 per dish. After an additional 24 to 48 hours the cells were  
scraped off the plate, spun down, and resuspended in a  
volume of 1 ml. After 3 freeze/thaw cycles trypsin was  
added to 0.05 mg/ml and lysates were incubated for 20 min.  
A dilution series of 10, 1 and 0.1 μl of this lysate was  
25 used to infect small dishes (6 cm) of CV1 cells, that had  
been pretreated with 12.5 μg/ml mycophenolic acid, 0.25  
mg/ml xanthin and 1.36 mg/ml hypoxanthine for 6 hours.  
Infected cells were cultured for 2 to 3 days, and  
subsequently stained with the monoclonal antibody NEA9301  
30 against gp120 and an alkaline phosphatase conjugated  
secondary antibody. Cells were incubated with 0.33 mg/ml  
NBT and 0.16 mg/ml BCIP in AP-buffer and finally overlaid  
with 1% agarose in PBS. Positive plaques were picked and

resuspended in 100  $\mu$ l Tris pH 9.0. The plaque purification was repeated once. To produce high titer stocks the infection was slowly scaled up. Finally, one large plate of Hela cells was infected with half of the virus of the previous round. Infected cells were detached in 3 ml of PBS, lysed with a Dounce homogenizer and cleared from larger debris by centrifugation. VPE-8 recombinant vaccinia stocks were kindly provided by the AIDS repository, Rockville, MD, and express HIV-1 IIIB gp120 under the 7.5 mixed early/late promoter (Earl et al., J. Virol., 65:31, 1991). In all experiments with recombinant vaccinia cells were infected at a multiplicity of infection of at least 10.

The following solution was used in this procedure:  
AP buffer (100 mM Tris HCl, pH 9.5, 100 mM NaCl, 5 mM  $MgCl_2$ )

#### Cell culture

The monkey kidney carcinoma cell lines CV1 and Cos7, the human kidney carcinoma cell line 293T, and the human cervix carcinoma cell line Hela were obtained from the American Tissue Typing Collection and were maintained in supplemented IMDM. They were kept on 10 cm tissue culture plates and typically split 1:5 to 1:20 every 3 to 4 days.

The following medium was used in this procedure:

Supplemented IMDM (90% Iscove's modified Dulbecco Medium, 10% calf serum, iron-complemented, heat inactivated 30 min 56°C, 0.3 mg/ml L-glutamine, 25  $\mu$ g/ml gentamycin 0.5 mM  $\beta$ -mercaptoethanol (pH adjusted with 5 M NaOH, 0.5 ml)).

#### Transfection

Calcium phosphate transfection of 293T cells was performed by slowly adding and under vortexing 10  $\mu$ g plasmid DNA in 250  $\mu$ l 0.25 M  $CaCl_2$  to the same volume of 2x HEBS buffer while vortexing. After incubation for 10 to 30 min at room temperature the DNA precipitate was added to a small dish of 50 to 70% confluent cells. In cotransfection

experiments with rev, cells were transfected with 10  $\mu$ g gp120IIIb, gp120IIIbrre, syngp120mnrrre or rTHY-1enveglrre and 10  $\mu$ g of pCMVrev or CDM7 plasmid DNA.

The following solutions were used in this procedure:

- 5 2x HEBS buffer (280 mM NaCl, 10 mM KCl, 1.5 mM sterile filtered); 0.25 mM  $\text{CaCl}_2$  (autoclaved).

#### Immunoprecipitation

- After 48 to 60 hours medium was exchanged and cells were incubated for additional 12 hours in Cys/Met-free  
10 medium containing 200  $\mu$ Ci of  $^{35}\text{S}$ -translabel. Supernatants were harvested and spun for 15 min at 3000 rpm to remove debris. After addition of protease inhibitors leupeptin, aprotinin and PMSF to 2.5  $\mu$ g/ml, 50  $\mu$ g/ml, 100  $\mu$ g/ml respectively, 1 ml of supernatant was incubated with either  
15 10  $\mu$ l of packed protein A sepharose alone (rTHY-1enveglrre) or with protein A sepharose and 3  $\mu$ g of a purified CD4/immunoglobulin fusion protein (kindly provided by Behring) (all gp120 constructs) at 4°C for 12 hours on a rotator. Subsequently the protein A beads were washed 5  
20 times for 5 to 15 min each time. After the final wash 10  $\mu$ l of loading buffer containing was added, samples were boiled for 3 min and applied on 7% (all gp120 constructs) or 10% (rTHY-1enveglrre) SDS polyacrylamide gels (TRIS pH 8.8 buffer in the resolving, TRIS pH 6.8 buffer in the stacking  
25 gel, TRIS-glycin running buffer, Maniatis et al., supra 1989). Gels were fixed in 10% acetic acid and 10 % methanol, incubated with Amplify for 20 min, dried and exposed for 12 hours.

- The following buffers and solutions were used in  
30 this procedure: Wash buffer (100 mM Tris, pH 7.5, 150 mM NaCl, 5 mM  $\text{CaCl}_2$ , 1% NP-40); 5x Running Buffer (125 mM Tris, 1.25 M Glycin, 0.5% SDS); Loading buffer (10 % glycerol, 4% SDS, 4%  $\beta$ -mercaptoethanol, 0.02 % bromphenol blue).

### Immunofluorescence

293T cells were transfected by calcium phosphate coprecipitation and analyzed for surface THY-1 expression after 3 days. After detachment with 1 mM EDTA/PBS, cells  
5 were stained with the monoclonal antibody OX-7 in a dilution of 1:250 at 4°C for 20 min, washed with PBS and subsequently incubated with a 1:500 dilution of a FITC-conjugated goat anti-mouse immunoglobulin antiserum. Cells were washed again, resuspended in 0.5 ml of a fixing solution, and  
10 analyzed on a EPICS XL cytofluorometer (Coulter).

The following solutions were used in this procedure: PBS (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.4 mM KH<sub>2</sub>PO<sub>4</sub>, pH adjusted to 7.4); Fixing solution (2% formaldehyde in PBS).

### ELISA

The concentration of gp120 in culture supernatants was determined using CD4-coated ELISA plates and goat anti-gp120 antisera in the soluble phase. Supernatants of 293T cells transfected by calcium phosphate were harvested after  
20 4 days, spun at 3000 rpm for 10 min to remove debris and incubated for 12 hours at 4°C on the plates. After 6 washes with PBS 100 µl of goat anti-gp120 antisera diluted 1:200 were added for 2 hours. The plates were washed again and incubated for 2 hours with a peroxidase-conjugated rabbit  
25 anti-goat IgG antiserum 1:1000. Subsequently the plates were washed and incubated for 30 min with 100 µl of substrate solution containing 2 mg/ml o-phenylenediamine in sodium citrate buffer. The reaction was finally stopped with 100 µl of 4 M sulfuric acid. Plates were read at 490  
30 nm with a Coulter microplate reader. Purified recombinant gp120IIIb was used as a control. The following buffers and solutions were used in this procedure: Wash buffer (0.1%

NP40 in PBS); Substrate solution (2 mg/ml o-phenylenediamine in sodium citrate buffer).

#### EXAMPLE 2

##### A Synthetic Green Fluorescent Protein Gene

5           The efficacy of codon replacement for gp120 suggests that replacing non-preferred codons with less preferred codons or preferred codons (and replacing less preferred codons with preferred codons) will increase expression in mammalian cells of other proteins, e.g., other eukaryotic  
10 proteins.

          The green fluorescent protein (GFP) of the jellyfish *Aequorea victoria* (Ward, Photochem. Photobiol. 4:1, 1979; Prasher et al., Gene 111:229, 1992; Cody et al., Biochem. 32:1212, 1993) has attracted attention recently for its  
15 possible utility as a marker or reporter for transfection and lineage studies (Chalfie et al., Science 263:802, 1994).

          Examination of a codon usage table constructed from the native coding sequence of GFP showed that the GFP codons favored either A or U in the third position. The bias in  
20 this case favors A less than does the bias of gp120, but is substantial. A synthetic gene was created in which the natural GFP sequence was re-engineered in much the same manner as for gp120 (FIG. 11; SEQ ID NO:40). In addition, the translation initiation sequence of GFP was replaced with  
25 sequences corresponding to the translational initiation consensus. The expression of the resulting protein was contrasted with that of the wild type sequence, similarly engineered to bear an optimized translational initiation consensus (FIG. 10B and FIG. 10C). In addition, the effect  
30 of inclusion of the mutation Ser 65→Thr, reported to improve excitation efficiency of GFP at 490 nm and hence preferred for fluorescence microscopy (Heim et al., Nature 373:663, 1995), was examined (FIG. 10D). Codon engineering conferred

960250-4527280  
a significant increase in expression efficiency (an  
concomitant percentage of cells apparently positive for  
transfection), and the combination of the Ser 65→Thr  
mutation and codon optimization resulted in a DNA segment  
5 encoding a highly visible mammalian marker protein (FIG.  
10D).

The above-described synthetic green fluorescent  
protein coding sequence was assembled in a similar manner as  
for gp120 from six fragments of approximately 120 bp each,  
10 using a strategy for assembly that relied on the ability of  
the restriction enzymes BsaI and BbsI to cleave outside of  
their recognition sequence. Long oligonucleotides were  
synthesized which contained portions of the coding sequence  
for GFP embedded in flanking sequences encoding EcoRI and  
15 BsaI at one end, and BamHI and BbsI at the other end. Thus,  
each oligonucleotide has the configuration EcoRI/BsaI/GFP  
fragment/BbsI/BamHI. The restriction site ends generated by  
the BsaI and BbsI sites were designed to yield compatible  
ends that could be used to join adjacent GFP fragments.  
20 Each of the compatible ends were designed to be unique and  
non-selfcomplementary. The crude synthetic DNA segments  
were amplified by PCR, inserted between EcoRI and BamHI in  
pUC9, and sequenced. Subsequently the intact coding  
sequence was assembled in a six fragment ligation, using  
25 insert fragments prepared with BsaI and BbsI. Two of six  
plasmids resulting from the ligation bore an insert of  
correct size, and one contained the desired full length  
sequence. Mutation of Ser65 to Thr was accomplished by  
standard PCR based mutagenesis, using a primer that  
30 overlapped a unique BssSI site in the synthetic GFP.

Codon optimization as a strategy for improved expression in mammalian cells

The data presented here suggest that coding sequence re-engineering may have general utility for the improvement of expression of mammalian and non-mammalian eukaryotic genes in mammalian cells. The results obtained here with three unrelated proteins: HIV gp120, the rat cell surface antigen Thy-1 and green fluorescent protein from *Aequorea victoria*, and human Factor VIII (see below) suggest that codon optimization may prove to be a fruitful strategy for improving the expression in mammalian cells of a wide variety of eukaryotic genes.

EXAMPLE III

Design of a Codon-Optimized Gene Expressing Human Factor VIII Lacking the Central B Domain

A synthetic gene was designed that encodes mature human Factor VIII lacking amino acid residues 760 to 1639, inclusive (residues 779 to 1658, inclusive, of the precursor). The synthetic gene was created by choosing codons corresponding to those favored by highly expressed human genes. Some deviation from strict adherence to the favored residue pattern was made to allow unique restriction enzyme cleavage sites to be introduced throughout the gene to facilitate future manipulations. For preparation of the synthetic gene the sequence was then divided into 28 segments of 150 basepairs, and a 29th segment of 161 basepairs.

The a synthetic gene expressing human Factor VIII lacking the central B domain was constructed as follows. Twenty-nine pairs of template oligonucleotides (see below) were synthesized. The 5' template oligos were 105 bases long and the 3' oligos were 104 bases long (except for the last 3' oligo, which was 125 residues long). The template

oligos were designed so that each annealing pair composed of one 5' oligo and one 3' oligo, created a 19 basepair double-stranded regions.

To facilitate the PCR and subsequent manipulations, the 5' ends of the oligo pairs were designed to be invariant over the first 18 residues, allowing a common pair of PCR primers to be used for amplification, and allowing the same PCR conditions to be used for all pairs. The first 18 residues of each 5' member of the template pair were cgc gaa ttc gga aga ccc (SEQ ID NO:110) and the first 18 residues of each 3' member of the template pair were: ggg gat cct cac gtc tca (SEQ ID NO:43).

Pairs of oligos were annealed and then extended and amplified by PCR in a reaction mixture as follows: templates were annealed at 200  $\mu$ g/ml each in PCR buffer (10 mM Tris-HCl, 1.5 mM  $MgCl_2$ , 50 mM KCl, 100  $\mu$ g/ml gelatin, pH 8.3). The PCR reactions contained 2 ng of the annealed template oligos, 0.5  $\mu$ g of each of the two 18-mer primers (described below), 200  $\mu$ M of each of the deoxynucleoside triphosphates, 10% by volume of DMSO and PCR buffer as supplied by Boehringer Mannheim Biochemicals, in a final volume of 50  $\mu$ l. After the addition of Taq polymerase (2.5 units, 0.5  $\mu$ l; Boehringer Mannheim Biochemicals) amplifications were conducted on a Perkin-Elmer Thermal Cycler for 25 cycles (94°C for 30 sec, 55°C for 30 sec, and 72°C for 30 sec). The final cycle was followed by a 10 minute extension at 72°C.

The amplified fragments were digested with EcoRI and BamHI (cleaving at the 5' and 3' ends of the fragments respectively) and ligated to a pUC9 derivative cut with EcoRI and BamHI.

Individual clones were sequenced and a collection of plasmids corresponding to the entire desired sequence was

identified. The clones were then assembled by multifragment ligation taking advantage of restriction sites at the 3' ends of the PCR primers, immediately adjacent to the amplified sequence. The 5' PCR primer contained a BbsI site, and the 3' PCR primer contained a BsmBI site, positioned so that cleavage by the respective enzymes preceded the first nucleotide of the amplified portion and left a 4 base 5' overhang created by the first 4 bases of the amplified portion. Simultaneous digestion with BbsI and BsmBI thus liberated the amplified portion with unique 4 base 5' overhangs at each end which contained none of the primer sequences. In general these overhangs were not self-complementary, allowing multifragment ligation reactions to produce the desired product with high efficiency. The unique portion of the first 28 amplified oligonucleotide pairs was thereby 154 basepairs, and after digestion each gave rise to a 150 bp fragment with unique ends. The first and last fragments were not manipulated in this manner, however, since they had other restriction sites designed into them to facilitate insertion of the assembled sequence into an appropriate mammalian expression vector. The actual assembly process proceeded as follows.

#### Assembly of the Synthetic Factor VIII Gene

##### Step 1: 29 Fragments Assembled to Form 10 Fragments.

The 29 pairs of oligonucleotides, which formed segments 1 to 29 when base-paired, are described below.

Plasmids carrying segments 1, 5, 9, 12, 16, 20, 24 and 27 were digested with EcoRI and BsmBI and the 170 bp fragments were isolated; plasmids bearing segments 2, 3, 6, 7, 10, 13, 17, 18, 21, 25, and 28 were digested with BbsI and BsmBI and the 170 bp fragments were isolated; and plasmids bearing segments 4, 8, 11, 14, 19, 22, 26 and 29 were digested with EcoRI and BbsI and the 2440 bp vector

fragment was isolated. Fragments bearing segments 1, 2, 3 and 4 were then ligated to generate segment "A"; fragments bearing segments 5, 6, 7 and 8 were ligated to generate segment "B"; fragments bearing segments 9, 10 and 11 were  
5 ligated to generate segment "C"; fragments bearing segments 12, 13, and 14 were ligated to generate segment "D"; fragments bearing segments 16, 17, 18 and 19 were ligated to generate segment "F"; fragments bearing segments 20, 21 and 22 were ligated to generate segment "G"; fragments bearing  
10 segments 24, 25 and 26 were ligated to generate segment "I"; and fragments bearing segments 27, 28 and 29 were ligated to generate segment "J".

Step 2: Assembly of the 10 resulting

Fragments from Step 1 to Three Fragments.

15 Plasmids carrying the segments "A", "D" and "G" were digested with EcoRI and BsmBI, plasmids carrying the segments B, 15, 23, and I were digested with BbsI and BsmBI, and plasmids carrying the segments C, F, and J were digested with EcoRI and BbsI. Fragments bearing segments A, B, and C  
20 were ligated to generate segment "K"; fragments bearing segments D, 15, and F were ligated to generate segment "O"; and fragments bearing segments G, 23, I, and J were ligated to generate segment "P".

Step 3: Assembly of the Final Three Pieces.

25 The plasmid bearing segment K was digested with EcoRI and BsmBI, the plasmid bearing segment O was digested with BbsI and BsmBI, and the plasmid bearing segment P was digested with EcoRI and BbsI. The three resulting fragments were ligated to generate segments.

Step 4: Insertion of the Synthetic Gene in a Mammalian Expression Vector.

The plasmid bearing segment S was digested with NheI and NotI and inserted between NheI and EagI sites of plasmid CD51NEg1 to generate plasmid cd51sf8b-.

Sequencing and Correction of the Synthetic Factor VIII Gene

After assembly of the synthetic gene it was discovered that there were two undesired residues encoded in the sequence. One was an Arg residue at 749, which is present in the GenBank sequence entry originating from Genentech but is not in the sequence reported by Genentech in the literature. The other was an Ala residue at 146, which should have been Pro. This mutation arose at an unidentified step subsequent to the sequencing of the 29 constituent fragments. The Pro749Arg mutation was corrected by incorporating the desired change in a PCR primer (ctg ctt ctg acg cgt gct ggg gtg gcg gga gtt; SEQ ID NO:44) that included the MluI site at position 2335 of the sequence below (sequence of HindIII to NotI segment) and amplifying between that primer and a primer (ctg ctg aaa gtc tcc agc tgc; SEQ ID NO:44) 5' to the SgrAI site at 2225. The SgrAI to MluI fragment was then inserted into the expression vector at the cognate sites in the vector, and the resulting correct sequence change verified by sequencing. The Pro146Ala mutation was corrected by incorporating the desired sequence change in an oligonucleotide (ggc agg tgc tta agg aga acg gcc cta tgg cca; SEQ ID NO:46) bearing the AflII site at residue 504, and amplifying the fragment resulting from PCR reaction between that oligo and the primer having sequence cgt tgt tct tca tac gcg tct ggg gct cct cgg ggc (SEQ ID NO:109), cutting the resulting PCR fragment with AflII and AvrII at (residue 989), inserting

the corrected fragment into the expression vector and confirming the construction by sequencing.

Construction of a Matched Native Gene Expressing Human Factor VIII Lacking the Central B Domain

5 A matched Factor VIII B domain deletion expression plasmid having the native codon sequence was constructed by introducing NheI at the 5' end of the mature coding sequence using primer cgc caa ggg cta gcc gcc acc aga aga tac tac ctg ggt (SEQ ID NO:47), amplifying between that primer and the  
10 primer att cgt agt tgg ggt tcc tct gga cag (corresponding to residues 1067 to 1093 of the sequence shown below), cutting with NheI and AflIII (residue 345 in the sequence shown below) and inserting the resulting fragment into an appropriately cleaved plasmid bearing native Factor VIII.

15 The B domain deletion was created by overlap PCR using ctg tat ttg atg aga acc g, (corresponding to residues 1813 to 1831 below) and caa gac tgg tgg ggt ggc att aaa ttg ctt t (SEQ ID NO:48) (2342 to 2372 on complement below) for the 5' end of the overlap, and aat gcc acc cca cca gtc ttg aaa cgc  
20 ca (SEQ ID NO:49) (2352 to 2380 on sequence below) and cat ctg gat att gca ggg ag (SEQ ID NO:50) (3145 to 3164). The products of the two individual PCR reactions were then mixed and reamplified by use of the outermost primers, the resulting fragment cleaved by Asp718 (KpnI isoschizomer,  
25 1837 on sequence below) and PflMI (3100 on sequence below), and inserted into the appropriately cleaved expression plasmid bearing native Factor VIII.

The complete sequence (SEQ ID NO:41) of the native human factor VIII gene deleted for the central B region is  
30 presented in Figure 12. The complete sequence (SEQ ID NO:42) of the synthetic Factor VIII gene deleted for the central B region is presented in Figure 13.

### Preparation and assay of expression plasmids

Two independent plasmid isolates of the native, and four independent isolates of the synthetic Factor VIII expression plasmid were separately propagated in bacteria and their DNA prepared by CsCl buoyant density centrifugation followed by phenol extraction. Analysis of the supernatants of COS cells transfected with the plasmids showed that the synthetic gene gave rise to approximately four times as much Factor VIII as did the native gene.

COS cells were then transfected with 5  $\mu$ g of each factor VIII construct per 6 cm dish using the DEAE-dextran method. At 72 hours post-transfection, 4 ml of fresh medium containing 10% calf serum was added to each plated. A sample of media was taken from each plate 12 hr later. Samples were tested by ELISA using mouse anti-human factor VIII light chain monoclonal antibody and peroxidase-conjugated goat anti-human factor VIII polyclonal antibody. Purified human plasma factor VIII was used as a standard. Cells transfected with the synthetic Factor VIII gene construct expressed  $138 \pm 20.2$  ng/ml (equivalent ng/ml non-deleted Factor VIII) of Factor VIII (n=4) while the cells transfected with the native Factor VIII gene expressed  $33.5 \pm 0.7$  ng/ml (equivalent ng/ml non-deleted Factor VIII) of Factor VIII (n=2).

The following template oligonucleotides were used for construction of the synthetic Factor VIII gene.

```

                                r1 bbs  1 for (gcta)
cgc gaa ttc gga aga ccc gct agc cgc cac          1 r1
ccg ccg cta cta cct ggg cgc cgt gga gct
gtc ctg gga cta cat gca gag cga cct ggg
cga gct ccc cgt gga (SEQ ID NO:51)
```

ggg gat cct cac gtc tca ggt ttt ctt gta  
cac cac gct ggt gtt gaa ggg gaa gct ctt  
ggg cac gcg ggg ggg gaa gcg ggc gtc cac  
ggg gag ctc gcc ca (SEQ ID NO:52)

1 bam

5 r1 bbs 2 for (aacc)

cgc gaa ttc gga aga ccc aac cct gtt cgt  
gga gtt cac cga cca cct gtt caa cat tgc  
caa gcc gcg ccc ccc ctg gat ggg cct gct  
ggg ccc cac cat cca (SEQ ID NO:53)

2 r1

10 ggg gat cct cac gtc tca gtg cag gct gac  
ggg gtg gct ggc cat gtt ctt cag ggt gat  
cac cac ggt gtc gta cac ctc ggc ctg gat  
ggt ggg gcc cag ca (SEQ ID NO:54)

2 bam

r1 bbs 3 for (gcac)

15 cgc gaa ttc gga aga ccc gca cgc cgt ggg  
cgt gag cta ctg gaa ggc cag cga ggg cgc  
cga gta cga cga cca gac gtc cca gcg cga  
gaa gga gga cga caa (SEQ ID NO:55)

3 r1

20 ggg gat cct cac gtc tca gct ggc cat agg  
gcc gtt ctc ctt aag cac ctg cca cac gta  
ggt gtg gct ccc ccc cgg gaa cac ctt gtc  
gtc ctc ctt ctc gc (SEQ ID NO:56)

3 bam

r1 bbs 4 for (cagc)

25 cgc gaa ttc gga aga ccc cag cga ccc cct  
gtg cct gac cta cag cta cct gag cca cgt  
gga cct ggt gaa gga tct gaa cag cgg gct  
gat cgg cgc cct gct (SEQ ID NO:57)

4 r1

ggg gat cct cac gtc tca gaa cag cag gat  
gaa ctt gtg cag ggt ctg ggt ttt ctc ctt  
ggc cag gct gcc ctc gcg aca cac cag cag  
ggc gcc gat cag cc (SEQ ID NO:58)

4 bam

5 r1 bbs 5 for (gttc)

cgc gaa ttc gga aga ccc gtt cgc cgt gtt  
cga cga ggg gaa gag ctg gca cag cga gac  
taa gaa cag cct gat gca gga ccg cga cgc  
cgc cag cgc ccg cgc (SEQ ID NO:59)

5 r1

10 ggg gat cct cac gtc tca gtg gca gcc gat  
cag gcc ggg cag gct gcg gtt cac gta gcc  
gtt aac ggt gtg cat ctt ggg cca ggc gcg  
ggc gct ggc ggc gt (SEQ ID NO:60)

5 bam

r1 bbs 6 for (ccac)

15 cgc gaa ttc gga aga ccc cca ccg caa gag  
cgt gta ctg gca cgt cat cgg cat ggg cac  
cac ccc tga ggt gca cag cat ctt cct gga  
ggg cca cac ctt cct (SEQ ID NO:61)

6 r1

20 ggg gat cct cac gtc tca cag ggt ctg ggc  
agt cag gaa ggt gat ggg gct gat ctc cag  
gct ggc ctg gcg gtg gtt gcg cac cag gaa  
ggt gtg gcc ctc ca (SEQ ID NO:62)

6 bam

r1 bbs 7 for (cctg)

25 cgc gaa ttc gga aga ccc cct gct gat gga  
cct agg cca gtt cct gct gtt ctg cca cat  
cag cag cca cca gca cga cgg cat gga ggc  
tta cgt gaa ggt gga (SEQ ID NO:63)

7 r1

ggg gat cct cac gtc tca gtc gtc gtc gta  
 gtc ctc ggc ctc ctc gtt gtt ctt cat gcg  
 cag ctg ggg ctc ctc ggg gca gct gtc cac  
 ctt cac gta agc ct (SEQ ID NO:64)

7 bam

5 r1 bbs 8 for (cgac)

cgc gaa ttc gga aga ccc cga cct gac cga  
 cag cga gat gga tgt cgt acg ctt cga cga  
 cga caa cag ccc cag ctt cat cca gat ccg  
 cag cgt ggc caa gaa (SEQ ID NO:65)

8 r1

10 ggg gat cct cac gtc tca tac tag cgg ggc  
 gta gtc cca gtc ctc ctc ctc ggc ggc gat  
 gta gtg cac cca ggt ctt agg gtg ctt ctt  
 ggc cac gct gcg ga (SEQ ID NO:66)

8 bam

r1 bbs 9 for (agta)

15 cgc gaa ttc gga aga ccc agt act ggc ccc  
 cga cga ccg cag cta caa gag cca gta cct  
 gaa caa cgg ccc cca gcg cat cgg ccg caa  
 gta caa gaa ggt gcg (SEQ ID NO:67)

9 r1

20 ggg gat cct cac gtc tca gag gat gcc gga  
 ctc gtg ctg gat ggc ctc gcg ggt ctt gaa  
 agt ctc gtc ggt gta ggc cat gaa gcg cac  
 ctt ctt gta ctt gc (SEQ ID NO:68)

9 bam

r1 bbs 10 for (cctc)

25 cgc gaa ttc gga aga ccc cct cgg ccc cct  
 gct gta cgg cga ggt ggg cga cac cct gct  
 gat cat ctt caa gaa cca ggc cag cag gcc  
 cta caa cat cta ccc (SEQ ID NO:69)

10 r1

ggg gat cct cac gtc tca ctt cag gtg ctt 10 bam  
cac gcc ctt ggg cag gcg gcg gct gta cag  
ggg gcg cac gtc ggt gat gcc gtg ggg gta  
gat gtt gta ggg cc (SEQ ID NO:70)

5 r1 bbs 11 for (gaag)  
cgc gaa ttc gga aga ccc gaa gga ctt ccc 11 r1  
cat cct gcc cgg cga gat ctt caa gta caa  
gtg gac cgt gac cgt gga gga cgg ccc cac  
caa gag cga ccc ccg (SEQ ID NO:71)

10 ggg gat cct cac gtc tca gcc gat cag tcc 11 bam  
gga ggc cag gtc gcg ctc cat gtt cac gaa  
gct gct gta gta gcg ggt cag gca gcg ggg  
gtc gct ctt ggt gg (SEQ ID NO:72)

r1 bbs 12 for (cggc)  
15 cgc gaa ttc gga aga ccc cgg ccc cct gct 12 r1  
gat ctg cta caa gga gag cgt gga cca gcg  
cgg caa cca gat cat gag cga caa gcg caa  
cgt gat cct gtt cag (SEQ ID NO:73)

ggg gat cct cac gtc tca agc ggg gtt ggg 12 bam  
20 cag gaa gcg ctg gat gtt ctc ggt cag ata  
cca gct gcg gtt ctc gtc gaa cac gct gaa  
cag gat cac gtt gc (SEQ ID NO:74)

r1 bbs 13 for (cgct)  
cgc gaa ttc gga aga ccc cgc tgg cgt gca 13 r1  
25 gct gga aga tcc cga gtt cca ggc cag caa  
cat cat gca cag cat caa cgg cta cgt gtt  
cga cag cct gca gct (SEQ ID NO:75)

ggg gat cct cac gtc tca cag gaa gtc ggt  
ctg ggc gcc gat gct cag gat gta cca gta  
ggc cac ctc atg cag gca cac gct cag ctg  
cag gct gtc gaa ca (SEQ ID NO:76)

13 bam

5 r1 bbs 14 for (cctg)

cgc gaa ttc gga aga ccc cct gag cgt gtt  
ctt ctc cgg gta tac ctt caa gca caa gat  
ggt gta cga gga cac cct gac cct gtt ccc  
ctt ctc cgg cga gac (SEQ ID NO:77)

14 r1

10 ggg gat cct cac gtc tca gtt gcg gaa gtc  
gct gtt gtg gca gcc cag aat cca cag gcc  
ggg gtt ctc cat aga cat gaa cac agt ctc  
gcc gga gaa ggg ga (SEQ ID NO:78)

14 bam

r1 bbs 15 for (caac)

15 cgc gaa ttc gga aga ccc caa ccg cgg cat  
gac tgc cct gct gaa agt ctc cag ctg cga  
caa gaa cac cgg cga cta cta cga gga cag  
cta cga gga cat ctc (SEQ ID NO:79)

15 r1

20 ggg gat cct cac gtc tca gcg gtg gcg gga  
gtt ttg gga gaa gga gcg ggg ctc gat ggc  
gtt gtt ctt gga cag cag gta ggc gga gat  
gtc ctc gta gct gt (SEQ ID NO:80)

15 bam

r1 bbs 16 for (ccgc)

25 cgc gaa ttc gga aga ccc ccg cag cac gcg  
tca gaa gca gtt caa cgc cac ccc ccc cgt  
gct gaa gcg cca cca gcg cga gat cac ccg  
cac cac cct gca aag (SEQ ID NO:81)

16 r1

ggg gat cct cac gtc tca gat gtc gaa gtc 16 bam  
ctc ctt ctt cat ctc cac gct gat ggt gtc  
gtc gta gtc gat ctc ctc ctg gtc gct ttg  
cag ggt ggt gcg gg (SEQ ID NO:82)

5 r1 bbs 17 for (catc)

cgc gaa ttc gga aga ccc cat cta cga cga 17 r1  
gga cga gaa cca gag ccc ccg ctc ctt cca  
aaa gaa aac ccg cca cta ctt cat cgc cgc  
cgt gga gcg cct gtg (SEQ ID NO:83)

10 ggg gat cct cac gtc tca ctg ggg cac gct 17 bam  
gcc gct ctg ggc gcg gtt gcg cag gac gtg  
ggg gct gct gct cat gcc gta gtc cca cag  
gcg ctc cac ggc gg (SEQ ID NO:84)

r1 bbs 18 for (ccag)

15 cgc gaa ttc gga aga ccc cca gtt caa gaa 18 r1  
ggt ggt gtt cca gga gtt cac cga cgg cag  
ctt cac cca gcc cct gta ccg cgg cga gct  
gaa cga gca cct ggg (SEQ ID NO:85)

20 ggg gat cct cac gtc tca ggc ttg gtt gcg 18 bam  
gaa ggt cac cat gat gtt gtc ctc cac ctc  
ggc gcg gat gta ggg gcc gag cag gcc cag  
gtg ctc gtt cag ct (SEQ ID NO:86)

r1 bbs 19 for (agcc)

25 cgc gaa ttc gga aga ccc agc ctc ccg gcc 19 r1  
cta ctc ctt cta ctc ctc cct gat cag cta  
cga gga gga cca gcg cca ggg cgc cga gcc  
ccg caa gaa ctt cgt (SEQ ID NO:87)

ggg gat cct cac gtc tca ctc gtc ctt ggt  
 ggg ggc cat gtg gtg ctg cac ctt cca gaa  
 gta ggt ctt agt ctc gtt ggg ctt cac gaa  
 gtt ctt gcg ggg ct (SEQ ID NO:88)

19 bam

5 r1 bbs 20 for (cgag)

cgc gaa ttc gga aga ccc cga gtt cga ctg  
 caa ggc ctg ggc cta ctt cag cga cgt gga  
 cct gga gaa gga cgt gca cag cgg cct gat  
 cgg ccc cct gct ggt (SEQ ID NO:89)

20 r1

10 ggg gat cct cac gtc tca gaa cag ggc aaa  
 ttc ctg cac agt cac ctg cct ccc gtg ggg  
 ggg gtt cag ggt gtt ggt gtg gca cac cag  
 cag ggg gcc gat ca (SEQ ID NO:90)

20 bam

r1 bbs 21 for (gttc)

15 cgc gaa ttc gga aga ccc gtt ctt cac cat  
 ctt cga cga gac taa gag ctg gta ctt cac  
 cga gaa cat gga gcg caa ctg ccg cgc ccc  
 ctg caa cat cca gat (SEQ ID NO:91)

21 r1

20 ggg gat cct cac gtc tca cag ggt gtc cat  
 gat gta gcc gtt gat ggc gtg gaa gcg gta  
 gtt ctc ctt gaa ggt ggg atc ttc cat ctg  
 gat gtt gca ggg gg (SEQ ID NO:92)

21 bam

r1 bbs 22 for (cctg)

25 cgc gaa ttc gga aga ccc cct gcc cgg cct  
 ggt gat ggc cca gga cca gcg cat ccg ctg  
 gta cct gct gtc tat ggg cag caa cga gaa  
 cat cca cag cat cca (SEQ ID NO:93)

22 r1

ggg gat cct cac gtc tca gta cag gtt gta 22 bam  
 cag ggc cat ctt gta ctc ctc ctt ctt gcg  
 cac ggt gaa aac gtg gcc gct gaa gtg gat  
 gct gtg gat gtt ct (SEQ ID NO:94)

5 r1 bbs 23 for (gtac)

cgc gaa ttc gga aga ccc gta ccc cgg cgt 23 r1  
 gtt cga gac tgt gga gat gct gcc cag caa  
 ggc cgg gat ctg gcg cgt gga gtg cct gat  
 cgg cga gca cct gca (SEQ ID NO:95)

10 ggg gat cct cac gtc tca gct ggc cat gcc 23 bam  
 cag ggg ggt ctg gca ctt gtt gct gta cac  
 cag gaa cag ggt gct cat gcc ggc gtg cag  
 gtg ctc gcc gat ca (SEQ ID NO:96)

r1 bbs 24 for (cagc)

15 cgc gaa ttc gga aga ccc cag cgg cca cat 24 r1  
 ccg cga ctt cca gat cac cgc cag cgg cca  
 gta cgg cca gtg ggc tcc caa gct ggc ccg  
 cct gca cta cag cgg (SEQ ID NO:97)

20 ggg gat cct cac gtc tca cat ggg ggc cag 24 bam  
 cag gtc cac ctt gat cca gga gaa ggg ctc  
 ctt ggt cga cca ggc gtt gat gct gcc gct  
 gta gtg cag gcg gg (SEQ ID NO:98)

r1 bbs 25 for (catg)

25 cgc gaa ttc gga aga ccc cat gat cat cca 25 r1  
 cgg cat caa gac cca ggg cgc ccg cca gaa  
 gtt cag cag cct gta cat cag cca gtt cat  
 cat cat gta ctc tct (SEQ ID NO:99)

ggg gat cct cac gtc tca gtt gcc gaa gaa 25 bam  
cac cat cag ggt gcc ggt gct gtt gcc gcg  
gta ggt ctg cca ctt ctt gcc gtc tag aga  
gta cat gat gat ga (SEQ ID NO:100)

5 r1 bbs 26 for (caac)

cgc gaa ttc gga aga ccc caa cgt gga cag 26 r1  
cag cgg cat caa gca caa cat ctt caa ccc  
ccc cat cat cgc ccg cta cat ccg cct gca  
ccc cac cca cta cag (SEQ ID NO:101)

10 ggg gat cct cac gtc tca gcc cag ggg cat 26 bam  
gct gca gct gtt cag gtc gca gcc cat cag  
ctc cat gcg cag ggt gct gcg gat gct gta  
gtg ggt ggg gtg ca (SEQ ID NO:102)

r1 bbs 27 for (gggc)

15 cgc gaa ttc gga aga ccc ggg cat gga gag 27 r1  
caa ggc cat cag cga cgc cca gat cac cgc  
ctc cag cta ctt cac caa cat gtt cgc cac  
ctg gag ccc cag caa (SEQ ID NO:103)

20 ggg gat cct cac gtc tca cca ctc ctt ggg 27 bam  
gtt gtt cac ctg ggg gcg cca ggc gtt gct  
gcg gcc ctg cag gtg cag gcg ggc ctt gct  
ggg gct cca ggt gg (SEQ ID NO:104)

r1 bbs 28 for (gtgg)

25 cgc gaa ttc gga aga ccc gtg gct gca ggt 28 r1  
gga ctt cca gaa aac cat gaa ggt gac tgg  
cgt gac cac cca ggg cgt caa gag cct gct  
gac cag cat gta cgt (SEQ ID NO:105)

ggg gat cct cac gtc tca ctt gcc gtt ttg 28 bam  
gaa gaa cag ggt cca ctg gtg gcc gtc ctg  
gct gct gct gat cag gaa ctc ctt cac gta  
cat gct ggt cag ca (SEQ ID NO:106)

5 r1 bbs 29 for (caag)

cgc gaa ttc gga aga ccc caa ggt gaa ggt 29 r1  
gtt cca ggg caa cca gga cag ctt cac acc  
ggt cgt gaa cag cct gga ccc ccc cct gct  
gac ccg cta cct gcg (SEQ ID NO:107)

10 ggg gat cct cac gtc tca gcg gcc gct tca 29 bam  
gta cag gtc ctg ggc ctc gca gcc cag cac  
ctc cat gcg cag ggc gat ctg gtg cac cca  
gct ctg ggg gtg gat gcg cag gta gcg ggt  
cag ca (SEQ ID NO:108)

15 The codon usage for the native and synthetic genes  
described above are presented in Tables 3 and 4,  
respectively.

TABLE 3: Codon Frequency of the Synthetic  
Factor VIII B Domain Deleted Gene

20	AA	Codon	Number	/1000	Fraction
	Gly	GGG	7.00	4.82	0.09
	Gly	GGA	1.00	0.69	0.01
	Gly	GGT	0.00	0.00	0.00
25	Gly	GGC	74.00	50.93	0.90
	Glu	GAG	81.00	55.75	0.96
	Glu	GAA	3.00	2.06	0.04
	Asp	GAT	4.00	2.75	0.05
30	Asp	GAC	78.00	53.68	0.95
	Val	GTG	77.00	52.99	0.88
	Val	GTA	2.00	1.38	0.02
	Val	GTT	2.00	1.38	0.02

	Val	GTC	7.00	4.82	0.08
	Ala	GCG	0.00	0.00	0.00
	Ala	GCA	0.00	0.00	0.00
5	Ala	GCT	3.00	2.06	0.04
	Ala	GCC	67.00	46.11	0.96
	Arg	AGG	2.00	1.38	0.03
	Arg	AGA	0.00	0.00	0.00
10	Ser	AGT	0.00	0.00	0.00
	Ser	AGC	97.00	66.76	0.81
	Lys	AAG	75.00	51.62	0.94
	Lys	AAA	5.00	3.44	0.06
15	Asn	AAT	0.00	0.00	0.00
	Asn	AAC	63.00	43.36	1.00
	Met	ATG	43.00	29.59	1.00
	Ile	ATA	0.00	0.00	0.00
20	Ile	ATT	2.00	1.38	0.03
	Ile	ATC	72.00	49.55	0.97
	Thr	ACG	2.00	1.38	0.02
	Thr	ACA	1.00	0.69	0.01
25	Thr	ACT	10.00	6.88	0.12
	Thr	ACC	70.00	48.18	0.84
	Trp	TGG	28.00	19.27	1.00
	End	TGA	1.00	0.69	1.00
30	Cys	TGT	1.00	0.69	0.05
	Cys	TGC	18.00	12.39	0.95
	End	TAG	0.00	0.00	0.00
	End	TAA	0.00	0.00	0.00
35	Tyr	TAT	2.00	1.38	0.03
	Tyr	TAC	66.00	45.42	0.97
	Leu	TTG	0.00	0.00	0.00
	Leu	TTA	0.00	0.00	0.00
40	Phe	TTT	1.00	0.69	0.01
	Phe	TTC	76.00	52.31	0.99
	Ser	TCG	1.00	0.69	0.01
	Ser	TCA	0.00	0.00	0.00
45	Ser	TCT	3.00	2.06	0.03
	Ser	TCC	19.00	13.08	0.16
	Arg	CGG	1.00	0.69	0.01
	Arg	CGA	0.00	0.00	0.00

	Arg	CGT	1.00	0.69	0.01
	Arg	CGC	69.00	47.49	0.95
5	Gln	CAG	62.00	42.67	0.93
	Gln	CAA	5.00	3.44	0.07
	His	CAT	1.00	0.69	0.02
	His	CAC	50.00	34.41	0.98
10	Leu	CTG	118.00	81.21	0.94
	Leu	CTA	3.00	2.06	0.02
	Leu	CTT	1.00	0.69	0.01
	Leu	CTC	3.00	2.06	0.02
15	Pro	CCG	4.00	2.75	0.05
	Pro	CCA	0.00	0.00	0.00
	Pro	CCT	3.00	2.06	0.04
	Pro	CCC	68.00	46.80	0.91

TABLE 4: Codon Frequency Table of the Native  
Factor VIII B Domain Deleted Gene

	AA	Codon	Number	/1000	Fraction
5					
	Gly	GGG	12.00	8.26	0.15
	Gly	GGA	34.00	23.40	0.41
	Gly	GGT	16.00	11.01	0.20
	Gly	GGC	20.00	13.76	0.24
10					
	Glu	GAG	33.00	22.71	0.39
	Glu	GAA	51.00	35.10	0.61
	Asp	GAT	55.00	37.85	0.67
	Asp	GAC	27.00	18.58	0.33
15					
	Val	GTG	29.00	19.96	0.33
	Val	GTA	19.00	13.08	0.22
	Val	GTT	17.00	11.70	0.19
	Val	GTC	23.00	15.83	0.26
20					
	Ala	GCG	2.00	1.38	0.03
	Ala	GCA	18.00	12.39	0.25
	Ala	GCT	31.00	21.34	0.44
	Ala	GCC	20.00	13.76	0.28
25					
	Arg	AGG	18.00	12.39	0.25
	Arg	AGA	22.00	15.14	0.30
	Ser	AGT	22.00	15.14	0.18
	Ser	AGC	24.00	16.52	0.20
30					
	Lys	AAG	32.00	22.02	0.40
	Lys	AAA	48.00	33.04	0.60
	Asn	AAT	38.00	26.15	0.60
	Asn	AAC	25.00	17.21	0.40
35					
	Met	ATG	43.00	29.59	1.00
	Ile	ATA	13.00	8.95	0.18
	Ile	ATT	36.00	24.78	0.49
	Ile	ATC	25.00	17.21	0.34
40					
	Thr	ACG	1.00	0.69	0.01
	Thr	ACA	23.00	15.83	0.28
	Thr	ACT	36.00	24.78	0.43
	Thr	ACC	23.00	15.83	0.28
45					
	Trp	TGG	28.00	19.27	1.00
	End	TGA	1.00	0.69	1.00

	Cys	TGT	7.00	4.82	0.37
	Cys	TGC	12.00	8.26	0.63
5	End	TAG	0.00	0.00	0.00
	End	TAA	0.00	0.00	0.00
	Tyr	TAT	41.00	28.22	0.60
	Tyr	TAC	27.00	18.58	0.40
10	Leu	TTG	20.00	13.76	0.16
	Leu	TTA	10.00	6.88	0.08
	Phe	TTT	45.00	30.97	0.58
	Phe	TTC	32.00	22.02	0.42
15	Ser	TCG	2.00	1.38	0.02
	Ser	TCA	27.00	18.58	0.22
	Ser	TCT	27.00	18.58	0.22
	Ser	TCC	18.00	12.39	0.15
20	Arg	CGG	6.00	4.13	0.08
	Arg	CGA	10.00	6.88	0.14
	Arg	CGT	7.00	4.82	0.10
	Arg	CGC	10.00	6.88	0.14
25	Gln	CAG	42.00	28.91	0.63
	Gln	CAA	25.00	17.21	0.37
	His	CAT	28.00	19.27	0.55
	His	CAC	23.00	15.83	0.45
30	Leu	CTG	36.00	24.78	0.29
	Leu	CTA	15.00	10.32	0.12
	Leu	CTT	24.00	16.52	0.19
	Leu	CTC	20.00	13.76	0.16
35	Pro	CCG	1.00	0.69	0.01
	Pro	CCA	32.00	22.02	0.43
	Pro	CCT	26.00	17.89	0.35
	Pro	CCC	15.00	10.32	0.20

#### Use

40           The synthetic genes of the invention are useful for  
expressing the a protein normally expressed in mammalian  
cells in cell culture (e.g. for commercial production of  
human proteins such as hGH, TPA, Factor VIII, and Factor  
IX). The synthetic genes of the invention are also useful  
45 for gene therapy. For example, a synthetic gene encoding a

selected protein can be introduced in to a cell which can  
express the protein to create a cell which can be  
administered to a patient in need of the protein. Such  
cell-based gene therapy techniques are well known to those  
5 skilled in the art, see, e.g., Anderson, et al., U.S. Patent  
No. 5,399,349; Mulligan and Wilson, U.S. Patent  
No. 5,460,959.

What is claimed is:

1. A synthetic gene encoding a protein normally expressed in an eukaryotic cell wherein at least one non-preferred or less preferred codon in a natural gene encoding said protein has been replaced by a preferred codon encoding the same amino acid, said synthetic gene being capable of expressing said protein at a level which is at least 110% of that expressed by said natural gene in an *in vitro* mammalian cell culture system under identical conditions.

2. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said protein at a level which is at least 150% of that expressed by said natural gene in an *in vitro* cell culture system under identical conditions.

3. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said protein at a level which is at least 200% of that expressed by said natural gene in an *in vitro* cell culture system under identical conditions.

4. The synthetic gene of claim 1 wherein said synthetic gene is capable of expressing said protein at a level which is at least 500% of that expressed by said natural gene in an *in vitro* cell culture system under identical conditions.

5. The synthetic gene of claim 1 wherein said synthetic gene comprises fewer than 5 occurrences of the sequence CG.

6. The synthetic gene of claim 1 wherein at least 10% of the codons in said natural gene are non-preferred codons.

5 7. The synthetic gene of claim 1 wherein at least 50% of the codons in said natural gene are non-preferred codons.

8. The synthetic gene of claim 1 wherein at least 50% of the non-preferred codons and less preferred codons present in said natural gene have been replaced by preferred  
10 codons.

9. The synthetic gene of claim 1 wherein at least 90% of the non-preferred codons and less preferred codons present in said natural gene have been replaced by preferred codons.

15 10. The synthetic gene of claim 1 wherein said protein is normally expressed by a mammalian cell.

11. The synthetic gene of claim 1 wherein said protein is a retroviral protein.

12. The synthetic gene of claim 1 wherein said  
20 protein is a lentiviral protein.

13. The synthetic gene of claim 11 wherein said protein is an HIV protein.

14. The synthetic gene of claim 13 wherein said  
25 protein is selected from the group consisting of gag, pol, and env.

15. The synthetic gene of claim 13 wherein said protein is gp120.

16. The synthetic gene of claim 13 wherein said protein is gp160.

5 17. The synthetic gene of claim 1 wherein said protein is a human protein.

18. The synthetic gene of claim 1 wherein said human protein is Factor VIII.

10 19. The synthetic gene of claim 1 wherein 20% of the codons are preferred codons.

20. The synthetic gene of claim 18 wherein said gene has the coding sequence present in SEQ ID NO:42.

21. The synthetic gene of claim 1 wherein said protein is green fluorescent protein.

15 22. The synthetic gene of claim 20 wherein said synthetic gene is capable of expressing said green fluorescent protein at a level which is at least 200% of that expressed by said natural gene in an *in vitro* mammalian cell culture system under identical conditions.

20 23. The synthetic gene of claim 20 wherein said synthetic gene is capable of expressing said green fluorescent protein at a level which is at least 1000% of that expressed by said natural gene in an *in vitro* mammalian cell culture system under identical conditions.

24. The synthetic gene of claim 21 having the sequence depicted in Figure 11 (SEQ ID NO:40).

25. An expression vector comprising the synthetic gene of claim 1.

5           26. The expression vector of claim 21, said expression vector being a mammalian expression vector.

27. A mammalian cell harboring with the synthetic gene of claim 1.

10           28. A method for preparing a synthetic gene encoding a protein normally expressed by mammalian cells, comprising identifying non-preferred and less-preferred codons in the natural gene encoding said protein and replacing one or more of said non-preferred and less-preferred codons with a preferred codon encoding the same  
15 amino acid as the replaced codon.

## HIGH LEVEL EXPRESSION OF PROTEINS

### Abstract of the Disclosure

The invention features a synthetic gene encoding a protein normally expressed in a mammalian cell wherein at least one non-preferred or less preferred codon in the natural gene encoding the protein has been replaced by a preferred codon encoding the same amino acid.

203353.B11

Syngpl20mn

1 CTCGAGATCC ATTGTGCTCT AAAGGAGATA CCCGGCCAGA CACCCTCACC  
 51 TCGGGTGCCC AGCTGCCCAG GCTGAGGCAA GAGAAGGCCA GAAACCATGC  
 101 CCATGGGGTC TGTGCAACCG CTGGCCACCT TGTACCTGCT GGGGATGCTG  
 151 GTCGCTTCCG TGCTAGCCAC CGAGAAGCTG TGGGTGACCG TGTACTACGG  
 201 CGTGCCCGTG TGAAGGAGG CCACCACCAC CCTGTTCTGC GCCAGCGACG  
 251 CCAAGGCGTA CGACACCGAG GTGCACAACG TGTGGGCCAC CCAGGCGTGC  
 301 GTGCCACCG ACCCAACCC CCAGGAGGTG GAGCTCGTGA ACGTGACCGA  
 351 GAACTTCAAC ATGTGGAAGA ACAACATGGT GGAGCAGATG CATGAGGACA  
 401 TCATCAGCCT GTGGGACCAG AGCCTGAAGC CCTGCGTGAA GCTGACCCCC  
 451 CTGTGCGTGA CCTGAACTG CACCGACCTG AGGAACACCA CCAACACCAA  
 501 CAACAGCACC GCAACAACA ACAGCAACAG CGAGGGCACC ATCAAGGGCG  
 551 GCGAGATGAA CAACTGCAGC TTCAACATCA CCACCAGCAT CCGCGACAAG  
 601 ATGCAGAAGG AGTACGCCCT GCTGTACAAG CTGGATATCG TGAGCATCGA  
 651 CAACGACAGC ACCAGCTACC GCCTGATCTC CTGCAACACC AGCGTGATCA  
 701 CCCAGGCCTG QCCCAAGATC AGCTTCGAGC CCATCCCCAT CCACTACTGC  
 751 GCCCCGCGCG GCTTCGCCAT CCTGAAGTGC AACGACAAGA AGTTCAGCGG  
 801 CAAGGGCAGC TGCAAGAACG TGAGCACCGT GCAGTGCACC CACGGCATCC  
 851 GGCCGGTGGT GAGCACCCAG CTCCTGCTGA ACGGCAGCCT GGCCGAGGAG  
 901 GAGGTGGTGA TCCGCAGCGA GAACTTCACC GACAACGCCA AGACCATCAT  
 951 CGTGACCTG AATGAGAGCG TGCAGATCAA CTGCACGCGT CCCAACTACA  
 1001 ACAAGCGCAA GCGCATCCAC ATCGGCCCCG GGCGCGCCTT CTACACCACC  
 1051 AAGAACATCA TCGGCACCAT CCGCCAGGCC CACTGCAACA TCTCTAGAGC  
 1101 CAAGTGGAAC GACACCCTGC GCCAGATCGT GAGCAAGCTG AAGGAGCAGT  
 1151 TCAAGAACAA GACCATCGTG TTCAACCAGA GCAGCGGCGG CGACCCCGAG  
 1201 ATCGTGATGC ACAGCTTCAA CTGCGGCGGC GAATTCTTCT ACTGCAACAC  
 1251 CAGCCCCCTG TTCAACAGCA CCTGGAACGG CAACAACACC TGGAACAACA  
 1301 CCACCGGCAG CAACAACAAT ATTACCCTCC AGTGCAAGAT CAAGCAGATC  
 1351 ATCAACATGT GGCAGGAGGT GGGCAAGGCC ATGTACGCCC CCCCCATCGA  
 1401 GGGCCAGATC CGGTGCAGCA GCAACATCAC CGGTCTGCTG CTGACCCGCG  
 1451 ACGGCGGCAA GGACACCGAC ACCAACGACA CCGAAATCTT CCGCCCCGGC

FIG 1  
(SHEET 1 OF 4)



syngp160mn

1 ACCGAGAAGC TGTGGGTGAC CGTGACTAC GCGGTGCCCC TGTGGAAGGA  
51 GGGCACCACC ACCCTGTTCT GCGCCAGCGA CGCCAAGGCG TACGACACCG  
101 AGGTGCACAA CGTGTGGGCC ACCCAGGCGT GCGTGCCAC CGACCCCAAC  
151 CCGCAGGAGG TGGAGCTCGT GAACGTGACC GAGAACTTCA ACATGTGGAA  
201 GAACAACATG CTGGAGCAGA TGCATGAGGA CATCATCAGC CTGTGGGACC  
251 AGAGCCTGAA GCGCTGCGTG AAGCTGACCC CCCTGTGCGT GACCCTCAAC  
301 TGCACCGACC TTAGGAACAC CACCAACACC AACAAACAGCA CCGCCACAA  
351 CAACAGCAAC AGCGAGGGCA CCATCAAGGG CGGCGAGATG AAGAACTGCA  
401 GCTTCAACAT CACCACCAGC ATCCCGGACA AGATCCAGAA GGAGTACGCC  
451 GTGCTGTACA AGCTGGATAT CGTGAGCATC CACAACGACA GCACCAGCTA  
501 CCGCCTGATC TCCTGCAACA CCAGCGTGAT CACCCAGGCC TGCCCCAAGA  
551 TCAGCTTCGA GCGCATCCCC ATCCACTACT GCGCCCCCGC CGGCTTCGCC  
601 ATCCTGAAGT GCAACGACAA GAAGTTCAGC GGCAAGGGCA GCTGCAAGAA  
651 CGTGACCACC CTGCAGTCCA CCCACGGCAT CCGGCCGGTG GTGAGCACCC  
701 ACCTCCTGCT GAACGGCAGC CTGGCCGAGG AGGAGGTGGT GATCCGAGC  
751 GAGAACTTCA CCGACAACGC CAAGACCATC ATCGTGACC TGAATGAGAG  
801 CGTGCAGATC AACTGCACGC GTCCCAACTA CAACAAGCGC AAGCGCATCC  
851 ACATCGGCCC CGGGCGCGCC TTCTACACCA CCAAGAACAT CATCGGCACC  
901 ATCCGCCAGG CCGACTGCAA CATCTCTAGA GCCAAGTGA ACGACACCCCT  
951 GCGCCAGATC GTGAGCAAGC TGAAGGAGCA GTTCAAGAAC AAGACCATCC  
1001 TGTTC AACCA GAGCAGCGGC GCGGACCCCG AGATCGTGAT GCACAGCTTC  
1051 AACTGCGGCG GCGAATTCTT CTAATGCAAC ACCAGCCCCC TGTTC AACAG  
1101 CACCTGGAAC GCGAACAA CACTGGAACAA CACCACCGGC AGCAACAACA  
1151 ATATTACCCT CCAGTGCAAG ATCAAGCAGA TCATCAACAT GTGGCAGGAG  
1201 GTGGGCAAGG CCATGTACGC CCCCCCATC GAGGGCCAGA TCCGGTGCAG  
1251 CAGCAACATC ACCGCTCTGC TGCTGACCCG CGACGGCGGC AAGGACACCG  
1301 ACACCAACGA CACCGAAATC TTCCGCCCCG GCGGCGGCGA CATGCGCGAC  
1351 AACTGGAGAT CTGAGCTGTA CAAGTACAAG GTGGTGACGA TCGAGCCCCCT  
1401 GCGCGTGGCC CCCACGAAGG CCAAGCGCCG CGTGGTGCAG CGCGAGAAGC

1451 GGGCCGCCAT CCGCGCCCTG TTCCTGGGCT TCCTGGGGGC GGCGGGCAGC  
1501 ACCATGGGGG CCGCCAGCGT GACCCTGACC GTGCAGGCCC GCCTGCTCCT  
1551 GAGCGGCATC GTGCAGCAGC AGAACAACCT CCTCCGCGCC ATCGAGGCCC  
1601 AGCAGCATAT GCTCCAGCTC ACCGTGTGGG GCATCAAGCA GCTCCAGGCC  
1651 CGCGTGCTGG CCGTGGAGCG CTACCTGAAG GACCAGCAGC TCCTGGGCTT  
1701 CTGGGGCTGC TCCGGCAAGC TGATCTGCAC CACACCGGTA CCTGGAACG  
1751 CCTCCTGGAG CAACAAGAGC CTGGACGACA TCTGGAACAA CATGACCTGG  
1801 ATGCAGTGGG ACGCGGAGAT CGATAACTAC ACCAGCCTGA TCTACAGCCT  
1851 GCTGGAGAAG AGCCAGACCC AGCAGGAGAA GAAAGAGCAG GAGCTGCTGG  
1901 AGCTGGACAA CCGGGCGAGC CTGTGGAACCT GGTTCGACAT CACCAACTGG  
1951 CTGTGGTACA TCAAAATCTT CATCATGATT GTGGGCGGCC TGGTGGGCCT  
2001 CCGCATCGTG TTCGCCGTGC TGAGCATCGT GAACCGCGTG CGCCAGGGCT  
2051 ACAGCCCCCT GAGCCTCCAG ACCCGGCCCC CCGTGCCGCG CGGGCCCGAC  
2101 CGCCCCGAGG GCATCGAGGA GGAGGGCGGC GAGCGCGACC GCGACACCAG  
2151 CGGCAGGCTC GTGCACGGCT TCCTGGCGAT CATCTGGGTC GACCTCCGCA  
2201 GCCTGTTCTT GTTCAGCTAC CACCACCGCG ACCTGCTGCT GATCGCCGCC  
2251 CGCATCGTGG AACTCCTAGG CCGCCGCGGC TGGGAGGTGC TGAAGTACTG  
2301 GTGGAACCTC CTCCAGTATT GGAGCCAGGA GCTGAAGTCC AGCGCCGTGA  
2351 GCCTGCTGAA CGCCACCGCC ATCGCCGTGG CCGAGGGCAC CGACCGCGTG  
2401 ATCGAGGTGC TCCAGAGGGC CGGGAGGGCG ATCCTGCACA TCCCCACCCG  
2451 CATCCGCCAG CGGCTCGAGA GGGCGCTGCT G (SEQ ID NO:35)

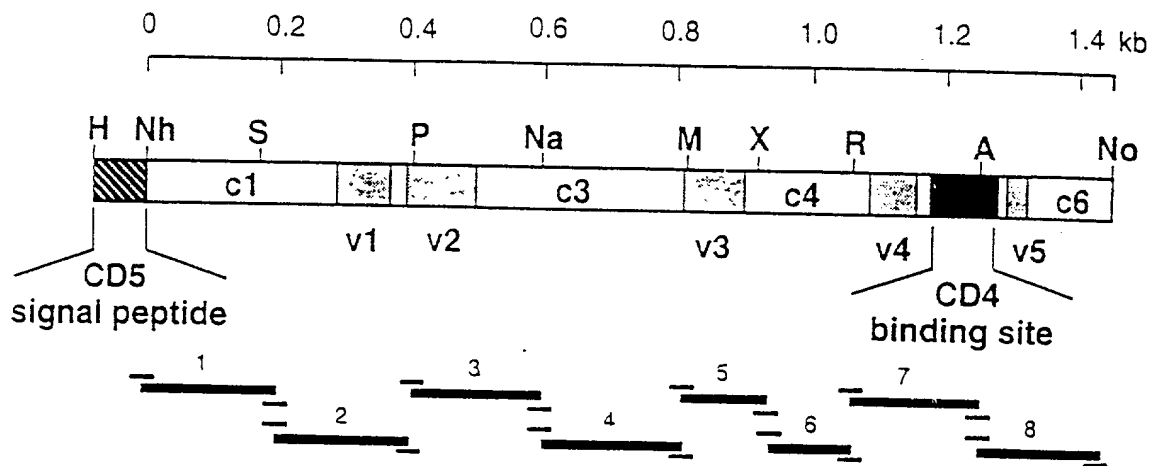


FIGURE 2

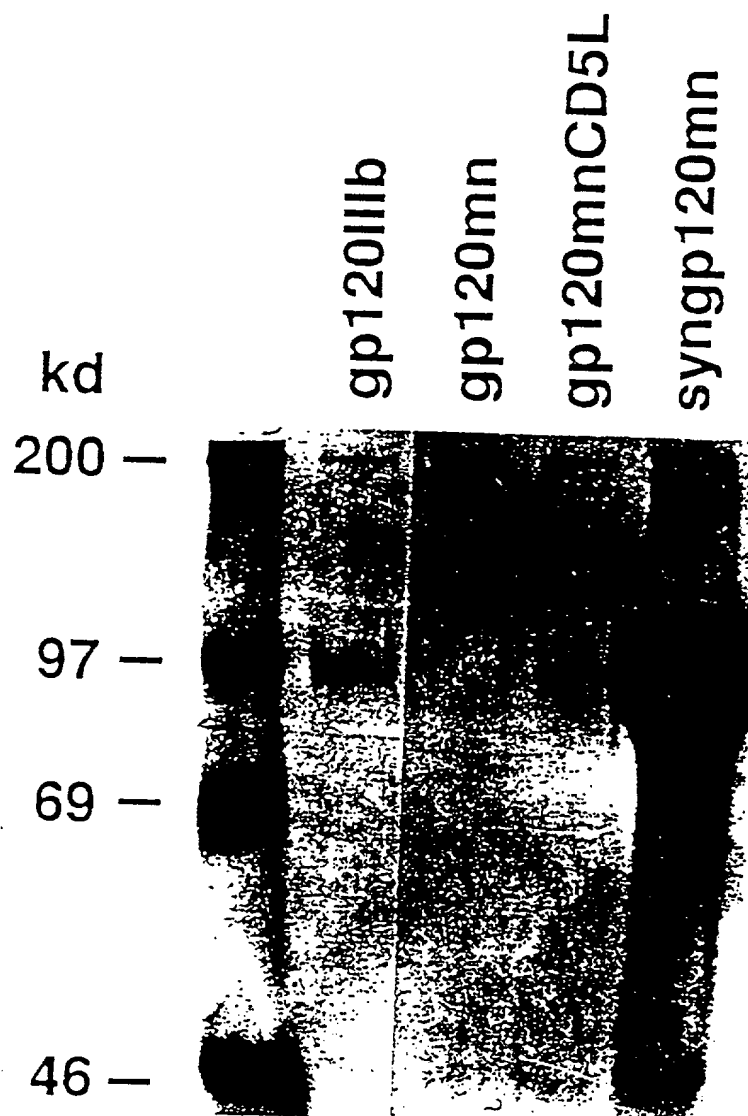


FIGURE 3

03/717611

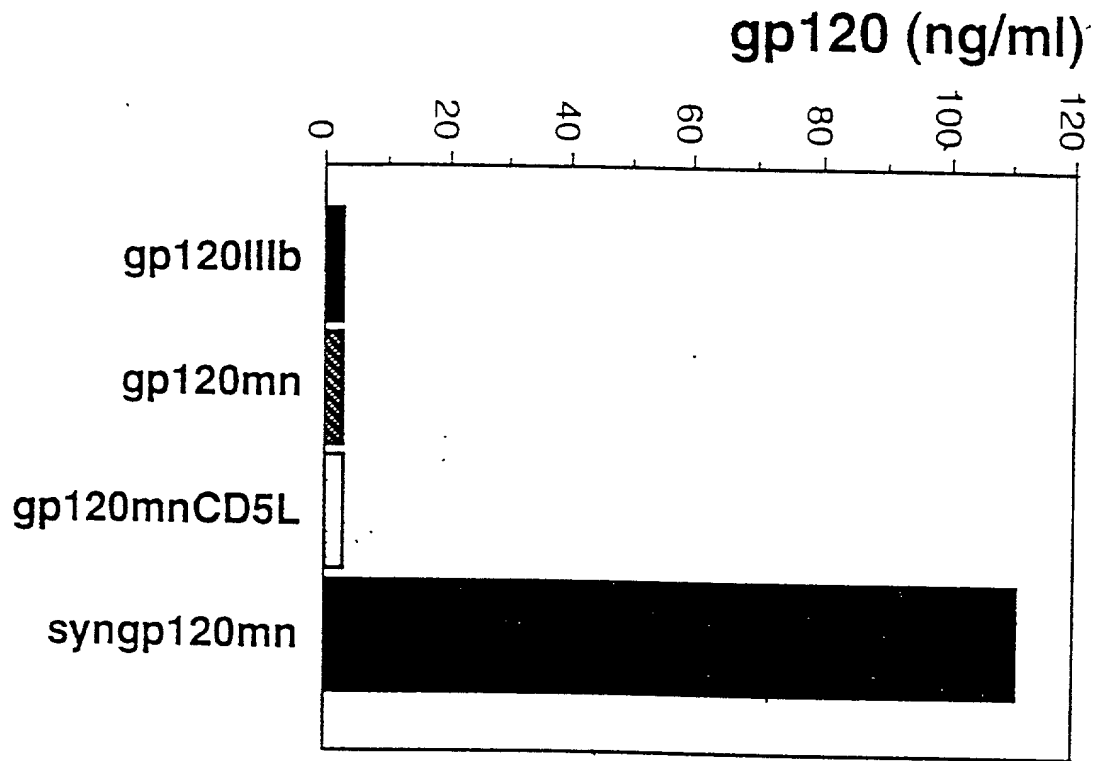
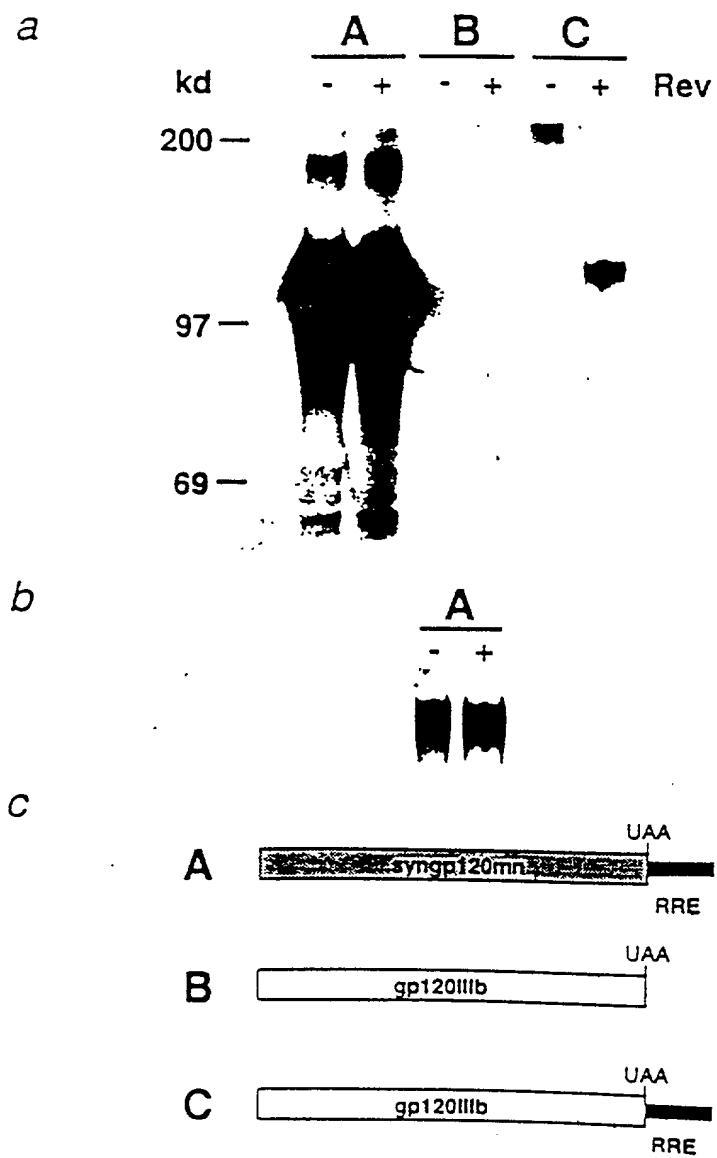


FIGURE 4

[illegible]

067150

FIGURE 6

	L	*
env	tta tga	tga tga
wt	ctg tga	tga tga

rTHY-1env

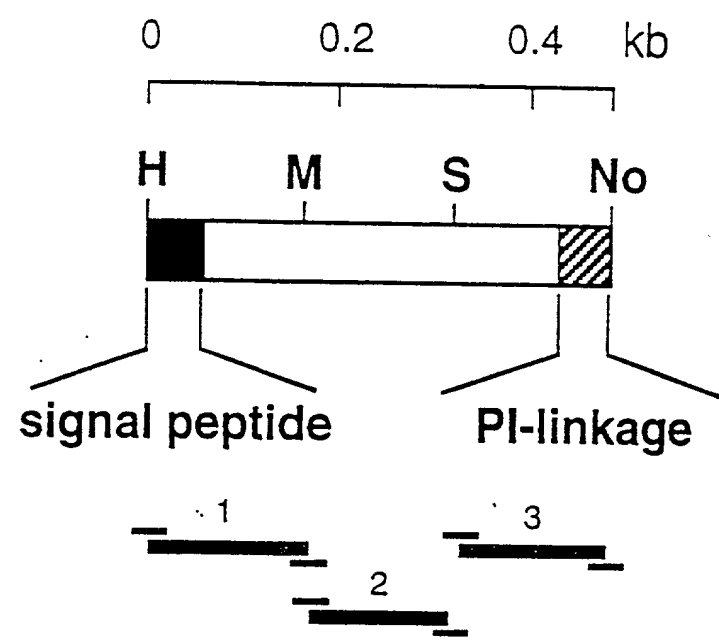


FIGURE 7

```

set.seed(12345)
N = 1000
n = 100
K = 10
n1 = n/2
n2 = n - n1
n3 = n/3
n4 = n - n1 - n3
n5 = n/4
n6 = n - n1 - n3 - n5

# Create data matrix
data = matrix(0, nrow = N, ncol = K)

# Fill data matrix with random values
for (i in 1:N) {
  for (j in 1:K) {
    data[i, j] = runif(1)
  }
}

# Split data into training and testing sets
train = data[1:n1, ]
test = data[n1+1:N, ]

# Calculate mean and standard deviation for each feature
trainMeans = apply(train, MARGIN = 2, FUN = mean)
trainSDs = apply(train, MARGIN = 2, FUN = sd)

# Calculate mean and standard deviation for each feature
testMeans = apply(test, MARGIN = 2, FUN = mean)
testSDs = apply(test, MARGIN = 2, FUN = sd)

# Calculate correlation matrix for training data
trainCorr = cor(train)

# Calculate correlation matrix for testing data
testCorr = cor(test)

# Calculate Pearson correlation coefficient between training and testing data
pearsonCorr = cor(trainMeans, testMeans)

# Calculate Spearman correlation coefficient between training and testing data
spearmanCorr = cor(rank(trainMeans), rank(testMeans))

# Calculate Kendall's tau correlation coefficient between training and testing data
kendallTau = cor(rank(trainMeans), rank(testMeans), method = "s")

# Calculate distance matrix for training data
trainDist = dist(train)

# Calculate distance matrix for testing data
testDist = dist(test)

# Calculate distance matrix for combined training and testing data
combinedDist = dist(rbind(train, test))

# Calculate distance matrix for training data using Manhattan distance
trainDistManhattan = dist(train, method = "manhattan")

# Calculate distance matrix for testing data using Manhattan distance
testDistManhattan = dist(test, method = "manhattan")

# Calculate distance matrix for combined training and testing data using Manhattan distance
combinedDistManhattan = dist(rbind(train, test), method = "manhattan")

# Calculate distance matrix for training data using Euclidean distance
trainDistEuclidean = dist(train, method = "euclidean")

# Calculate distance matrix for testing data using Euclidean distance
testDistEuclidean = dist(test, method = "euclidean")

# Calculate distance matrix for combined training and testing data using Euclidean distance
combinedDistEuclidean = dist(rbind(train, test), method = "euclidean")

# Calculate distance matrix for training data using Mahalanobis distance
trainDistMahalanobis = dist(train, method = "mahalanobis", diag = TRUE)

# Calculate distance matrix for testing data using Mahalanobis distance
testDistMahalanobis = dist(test, method = "mahalanobis", diag = TRUE)

# Calculate distance matrix for combined training and testing data using Mahalanobis distance
combinedDistMahalanobis = dist(rbind(train, test), method = "mahalanobis", diag = TRUE)

# Calculate distance matrix for training data using Cosine distance
trainDistCosine = dist(train, method = "cosine")

# Calculate distance matrix for testing data using Cosine distance
testDistCosine = dist(test, method = "cosine")

# Calculate distance matrix for combined training and testing data using Cosine distance
combinedDistCosine = dist(rbind(train, test), method = "cosine")

# Calculate distance matrix for training data using Jaccard distance
trainDistJaccard = dist(train, method = "jaccard")

# Calculate distance matrix for testing data using Jaccard distance
testDistJaccard = dist(test, method = "jaccard")

# Calculate distance matrix for combined training and testing data using Jaccard distance
combinedDistJaccard = dist(rbind(train, test), method = "jaccard")

# Calculate distance matrix for training data using Hamming distance
trainDistHamming = dist(train, method = "hamming")

# Calculate distance matrix for testing data using Hamming distance
testDistHamming = dist(test, method = "hamming")

# Calculate distance matrix for combined training and testing data using Hamming distance
combinedDistHamming = dist(rbind(train, test), method = "hamming")

# Calculate distance matrix for training data using Levenshtein distance
trainDistLevenshtein = dist(train, method = "levenshtein")

# Calculate distance matrix for testing data using Levenshtein distance
testDistLevenshtein = dist(test, method = "levenshtein")

# Calculate distance matrix for combined training and testing data using Levenshtein distance
combinedDistLevenshtein = dist(rbind(train, test), method = "levenshtein")

# Calculate distance matrix for training data using Dynamic Time Warping distance
trainDistDTW = dist(train, method = "dtw")

# Calculate distance matrix for testing data using Dynamic Time Warping distance
testDistDTW = dist(test, method = "dtw")

# Calculate distance matrix for combined training and testing data using Dynamic Time Warping distance
combinedDistDTW = dist(rbind(train, test), method = "dtw")

# Calculate distance matrix for training data using Wasserstein distance
trainDistWasserstein = dist(train, method = "wasserstein")

# Calculate distance matrix for testing data using Wasserstein distance
testDistWasserstein = dist(test, method = "wasserstein")

# Calculate distance matrix for combined training and testing data using Wasserstein distance
combinedDistWasserstein = dist(rbind(train, test), method = "wasserstein")

# Calculate distance matrix for training data using Earth Mover's distance
trainDistEMD = dist(train, method = "emd")

# Calculate distance matrix for testing data using Earth Mover's distance
testDistEMD = dist(test, method = "emd")

# Calculate distance matrix for combined training and testing data using Earth Mover's distance
combinedDistEMD = dist(rbind(train, test), method = "emd")

# Calculate distance matrix for training data using Manhattan distance with weights
trainDistManhattanW = dist(train, method = "manhattan", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Manhattan distance with weights
testDistManhattanW = dist(test, method = "manhattan", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Manhattan distance with weights
combinedDistManhattanW = dist(rbind(train, test), method = "manhattan", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Euclidean distance with weights
trainDistEuclideanW = dist(train, method = "euclidean", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Euclidean distance with weights
testDistEuclideanW = dist(test, method = "euclidean", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Euclidean distance with weights
combinedDistEuclideanW = dist(rbind(train, test), method = "euclidean", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Mahalanobis distance with weights
trainDistMahalanobisW = dist(train, method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), diag = TRUE)

# Calculate distance matrix for testing data using Mahalanobis distance with weights
testDistMahalanobisW = dist(test, method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), diag = TRUE)

# Calculate distance matrix for combined training and testing data using Mahalanobis distance with weights
combinedDistMahalanobisW = dist(rbind(train, test), method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), diag = TRUE)

# Calculate distance matrix for training data using Cosine distance with weights
trainDistCosineW = dist(train, method = "cosine", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Cosine distance with weights
testDistCosineW = dist(test, method = "cosine", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Cosine distance with weights
combinedDistCosineW = dist(rbind(train, test), method = "cosine", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Jaccard distance with weights
trainDistJaccardW = dist(train, method = "jaccard", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Jaccard distance with weights
testDistJaccardW = dist(test, method = "jaccard", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Jaccard distance with weights
combinedDistJaccardW = dist(rbind(train, test), method = "jaccard", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Hamming distance with weights
trainDistHammingW = dist(train, method = "hamming", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Hamming distance with weights
testDistHammingW = dist(test, method = "hamming", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Hamming distance with weights
combinedDistHammingW = dist(rbind(train, test), method = "hamming", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Levenshtein distance with weights
trainDistLevenshteinW = dist(train, method = "levenshtein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Levenshtein distance with weights
testDistLevenshteinW = dist(test, method = "levenshtein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Levenshtein distance with weights
combinedDistLevenshteinW = dist(rbind(train, test), method = "levenshtein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Dynamic Time Warping distance with weights
trainDistDTWW = dist(train, method = "dtw", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Dynamic Time Warping distance with weights
testDistDTWW = dist(test, method = "dtw", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Dynamic Time Warping distance with weights
combinedDistDTWW = dist(rbind(train, test), method = "dtw", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Wasserstein distance with weights
trainDistWassersteinW = dist(train, method = "wasserstein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Wasserstein distance with weights
testDistWassersteinW = dist(test, method = "wasserstein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Wasserstein distance with weights
combinedDistWassersteinW = dist(rbind(train, test), method = "wasserstein", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Earth Mover's distance with weights
trainDistEMDW = dist(train, method = "emd", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for testing data using Earth Mover's distance with weights
testDistEMDW = dist(test, method = "emd", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for combined training and testing data using Earth Mover's distance with weights
combinedDistEMDW = dist(rbind(train, test), method = "emd", weights = c(1, 2, 3, 4, 5, 6))

# Calculate distance matrix for training data using Manhattan distance with weights and scaling
trainDistManhattanWS = dist(train, method = "manhattan", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for testing data using Manhattan distance with weights and scaling
testDistManhattanWS = dist(test, method = "manhattan", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for combined training and testing data using Manhattan distance with weights and scaling
combinedDistManhattanWS = dist(rbind(train, test), method = "manhattan", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for training data using Euclidean distance with weights and scaling
trainDistEuclideanWS = dist(train, method = "euclidean", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for testing data using Euclidean distance with weights and scaling
testDistEuclideanWS = dist(test, method = "euclidean", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for combined training and testing data using Euclidean distance with weights and scaling
combinedDistEuclideanWS = dist(rbind(train, test), method = "euclidean", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for training data using Mahalanobis distance with weights and scaling
trainDistMahalanobisWS = dist(train, method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE, diag = TRUE)

# Calculate distance matrix for testing data using Mahalanobis distance with weights and scaling
testDistMahalanobisWS = dist(test, method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE, diag = TRUE)

# Calculate distance matrix for combined training and testing data using Mahalanobis distance with weights and scaling
combinedDistMahalanobisWS = dist(rbind(train, test), method = "mahalanobis", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE, diag = TRUE)

# Calculate distance matrix for training data using Cosine distance with weights and scaling
trainDistCosineWS = dist(train, method = "cosine", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for testing data using Cosine distance with weights and scaling
testDistCosineWS = dist(test, method = "cosine", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for combined training and testing data using Cosine distance with weights and scaling
combinedDistCosineWS = dist(rbind(train, test), method = "cosine", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for training data using Jaccard distance with weights and scaling
trainDistJaccardWS = dist(train, method = "jaccard", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for testing data using Jaccard distance with weights and scaling
testDistJaccardWS = dist(test, method = "jaccard", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for combined training and testing data using Jaccard distance with weights and scaling
combinedDistJaccardWS = dist(rbind(train, test), method = "jaccard", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for training data using Hamming distance with weights and scaling
trainDistHammingWS = dist(train, method = "hamming", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix for testing data using Hamming distance with weights and scaling
testDistHammingWS = dist(test, method = "hamming", weights = c(1, 2, 3, 4, 5, 6), scale = TRUE)

# Calculate distance matrix
```

FIGURE 8

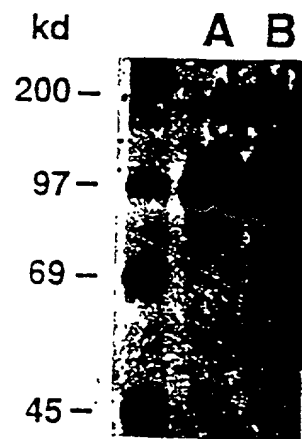
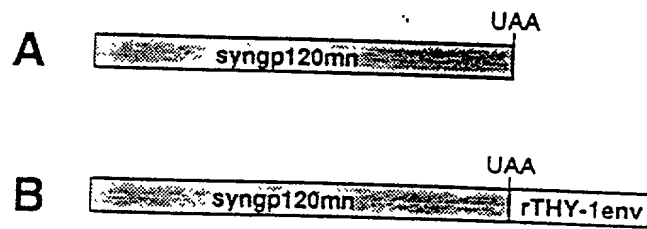
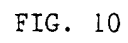
*a**b*

FIGURE 9



1 GAATTCACGC GTAAGCTTGC CGCCACCATG GTGAGCAAGG GCGAGGAGCT  
51 GTTCACCGGG GTGGTGCCCA TCCTGGTCGA GCTGGACGGC GACGTGAACG  
101 GCCACAAGTT CAGCGTGTCC GGCGAGGGCG AGGGCGATGC CACCTACGGC  
151 AAGCTGACCC TGAAGTTCAT CTGCACCACC GGCAAGCTGC CCGTGCCCTG  
201 GCCCACCCTC GTGACCACCT TCAGCTACGG CGTGCAGTGC TTCAGCCGCT  
251 ACCCCGACCA CATGAAGCAG CACGACTTCT TCAAGTCCGC CATGCCCCGAA  
301 GGCTACGTCC AGGAGCGCAC CATCTTCTTC AAGGACGACG GCAACTACAA  
351 GACCCGCGCC GAGGTGAAGT TCGAGGGCGA CACCCTGGTG AACCGCATCG  
401 AGCTGAAGGG CATCGACTTC AAGGAGGACG GCAACATCCT GGGGCACAAG  
451 CTGGAGTACA ACTACAACAG CCACAACGTC TATATCATGG CCGACAAGCA  
501 GAAGAACGGC ATCAAGGTGA ACTTCAAGAT CCGCCACAAC ATCGAGGACG  
551 GCAGCGTGCA GCTCGCCGAC CACTACCAGC AGAACACCCC CATCGGCGAC  
601 GGCCCCGTGC TGCTGCCCCG CAACCACTAC CTGAGCACCC AGTCCGCCCT  
651 GAGCAAAGAC CCCAACGAGA AGCGCGATCA CATGGTCCTG CTGGAGTTCG  
701 TGACCGCCGC CGGGATCACT CACGGCATGG ACGAGCTGTA CAAGTAAAGC  
751 GGCCGCGGAT CC (SEQ ID NO: 40)

FIG. 11

Native Factor VIII B domain deleted gene segment inserted in the expression vector

```

1  AAGCTTAAAC CATGCCCATG GGGTCTCTGC AACCGCTGGC CACCTTGTAC
51 CTGCTGGGGA TGCTGGTCGC TTCCGTGCTA GCCGCCACCA GAAGATACTA
101 CCTGGGTGCA GTGGAAGTGT CATGGGACTA TATGCAAAGT GATCTCCGTG
151 AGCTGCCTGT GGACGCAAGA TTTCTCCTA GAGTGCCAAA ATCTTTTCCA
201 TTCAACACCT CAGTCGTGTA CAAAAAGACT CTGTTTGTAG AATTCACGGA
251 TCACCTTTTC AACATCGCTA AGCCAAGGCC ACCCTGGATG GGTCTGCTAG
301 GTCCTACCAT CCAGGCTGAG GTTTATGATA CAGTGGTCAT TACACTTAAG
351 AACATGGCTT CCCATCCTGT CAGTCTTCAT GCTGTTGGTG TATCCTACTG
401 GAAAGCTTCT GAGGGAGCTG AATATGATGA TCAGACCAGT CAAAGGGAGA
451 AAGAAGATGA TAAAGTCTTC CCTGGTGGAA GCCATACATA TGTCTGGCAG
501 GTCCTGAAAG AGAATGGTCC AATGGCCTCT GACCCACTGT GCCTTACCTA
551 CTCATATCTT TCTCATGTGG ACCTGGTAAA AGACTTGAAT TCAGGCCCTCA
601 TTGGAGCCCT ACTAGTATGT AGAGAAGGGA GTCTGGCCAA GGAAAAGACA
651 CAGACCTTGC ACAAATTTAT ACTACTTTTT GCTGTATTTG ATGAAGGGAA
701 AAGTTGGCAC TCAGAAACAA AGAACTCCTT GATGCAGGAT AGGGATGCTG
751 CATCTGCTCG GGCCTGGCCT AAAATGCACA CAGTCAATGG TTATGTAAAC
801 AGGTCTCTGC CAGGTCTGAT TGGATGCCAC AGGAAATCAG TCTATTGGCA
851 TGTGATTGGA ATGGGCACCA CTCCTGAAGT GCACTCAATA TTCCTCGAAG
901 GTCACACATT TCTTGTGAGG AACCATCGCC AGGCGTCCTT GGAAATCTCG
951 CCAATAACTT TCCTTACTGC TCAAACACTC TTGATGGACC TTGGACAGTT
1001 TCTACTGTTT TGTCATATCT CTTCCACCA ACATGATGGC ATGGAAGCTT
1051 ATGTCAAAGT AGACAGCTGT CCAGAGGAAC CCCAACTACG AATGAAAAAT
1101 AATGAAGAAG CGGAAGACTA TGATGATGAT CTTACTGATT CTGAAATGGA
1151 TGTGGTCAGG TTTGATGATG ACAAATCTCC TTCCTTTATC CAAATTCGCT
1201 CAGTTGCCAA GAAGCATCCT AAAACTTGGG TACATTACAT TGCTGCTGAA
1251 GAGGAGGACT GGGACTATGC TCCCTTAGTC CTCGCCCCCG ATGACAGAAG
1301 TTATAAAAGT CAATATTTGA ACAATGGCCC TCAGCGGATT GGTAGGAAGT
1351 ACAAAAAAGT CCGATTTATG GCATACACAG ATGAAACCTT TAAGACTCGT
1401 GAAGCTATTG AGCATGAATC AGGAATCTTG GGACCTTTAC TTTATGGGGA
1451 AGTTGGAGAC ACACTGTTGA TTATATTTAA GAATCAAGCA AGCAGACCAT
1501 ATAACATCTA CCCTCACGGA ATCACTGATG TCCGTCCTTT GTATTCAAGG
1551 AGATTACCAA AAGGTGTAAA ACATTTGAAG GATTTTCCAA TTCTGCCAGG
1601 AGAAATATTC AAATATAAAT GGACAGTGAC TGTAAGAAGT GGGCCAACTA
1651 AATCAGATCC TCGGTGCCTG ACCCGCTATT ACTCTAGTTT CGTTAATATG
1701 GAGAGAGATC TAGCTTCAGG ACTCATTTGG CCTCTCCTCA TCTGCTACAA
1751 AGAATCTGTA GATCAAAGAG GAAACCAGAT AATGTCAGAC AAGAGGAATG
1801 TCATCCTGTT TTCTGTATTT GATGAGAACC GAAGCTGGTA CCTCACAGAG
1851 AATATACAAC GCTTTCTCCC CAATCCAGCT GGAGTGCAGC TTGAGGATCC
1901 AGAGTTCCAA GCCTCCAACA TCATGCACAG CATCAATGGC TATGTTTTTG
1951 ATAGTTTGCA GTTGTCAATT TGTTCATG AGGTGGCATA CTGGTACATT
2001 CTAAGCATTG GAGCACAGAC TGACTTCCTT TCTGTCTTCT TCTCTGGATA
2051 TACCTTCAA CACAAAATGG TCTATGAAGA CACACTCACC CTATTTCCAT
2101 TCTCAGGAGA AACTGTCTTC ATGTCGATGG AAAACCCAGG TCTATGGATT
2151 CTGGGGTGCC ACAACTCAGA CTTTCGGAAC AGAGGCATGA CCGCCTTACT
2201 GAAGGTTTCT AGTTGTGACA AGAACACTGG TGATTATTAC GAGGACAGTT
2251 ATGAAGATAT TTCAGCATAT TTGCTGAGTA AAAACAATGC CATTGAACCA
2301 AGAAGCTTCT CCCAGAATTC AAGACACCCCT AGCACTAGGC AAAAGCAATT
2351 TAATGCCACC CCACCAGTCT TGAACGCCA TCAACGGGAA ATAACTCGTA
2401 CTACTCTTCA GTCAGATCAA GAGGAAATTG ACTATGATGA TACCATATCA
2451 GTTGAAATGA AGAAGGAAGA TTTTGACATT TATGATGAGG ATGAAAATCA
2501 GAGCCCCCGC AGCTTTCAA AGAAAACACG ACCTATTTT ATTGCTGCAG
2551 TGGAGAGGCT CTGGGATTAT GGGATGAGTA GCTCCCCACA TGTCTAAGA
2601 AACAGGGCTC AGAGTGGCAG TGTCCCTCAG TTCAAGAAAG TTGTTTTCCA
2651 GGAATTTACT GATGGCTCCT TTAATCAGCC CTTATACCGT GGAGAACTAA
2701 ATGAACATTT GGGACTCCTG GGGCCATATA TAAGAGCAGA AGTTGAAGAT

```

Fig. 12

2751 AATATCATGG TAACTTTCAG AAATCAGGCC TCTCGTCCCT ATTCCTTCTA  
 2801 TTCTAGCCTT ATTTCTTATG AGGAAGATCA GAGGCAAGGA GCAGAACCTA  
 2851 GAAAAAACTT TGTCAGCCTT AATGAAACCA AAACCTTACTT TTGGAAAGTG  
 2901 CAACATCATA TGGCACCAC TAAAGATGAG TTTGACTGCA AAGCCTGGGC  
 2951 TTATTTCTCT GATGTTGACC TGGAAAAAGA TGTGCACTCA GGCCTGATTG  
 3001 GACCCCTTCT GGTCTGCCAC ACTAACACAC TGAACCCTGC TCATGGGAGA  
 3051 CAAGTGACAG TACAGGAATT TGCTCTGTTT TTCACCATCT TTGATGAGAC  
 3101 CAAAAGCTGG TACTTCACTG AAAATATGGA AAGAACTGC AGGGCTCCCT  
 3151 GCAATATCCA GATGGAAGAT CCCACTTTTA AAGAGAATTA TCGCTTCCAT  
 3201 GCAATCAATG GCTACATAAT GGATACACTA CCTGGCTTAG TAATGGCTCA  
 3251 GGATCAAAGG ATTCGATGGT ATCTGCTCAG CATGGGCAGC AATGAAAACA  
 3301 TCCATTCTAT TCATTTTCACT GGACATGTGT TCACTGTACG AAAAAAGAG  
 3351 GAGTATAAAA TGGCACTGTA CAATCTCTAT CCAGGTGTTT TTGAGACAGT  
 3401 GGAAATGTTA CCATCCAAAG CTGGAATTTG GCGGGTGGAA TGCCTTATTG  
 3451 GCGAGCATCT ACATGCTGGG ATGAGCACAC TTTTCTGGT GTACAGCAAT  
 3501 AAGTGTGAGA CTCCCCTGGG AATGGCTTCT GGACACATTA GAGATTTTCA  
 3551 GATTACAGCT TCAGGACAAT ATGGACAGTG GGCCCCAAAG CTGGCCAGAC  
 3601 TTCATTATTC CGGATCAATC AATGCCTGGA GCACCAAGGA GCCCTTTTCT  
 3651 TGGATCAAGG TGGATCTGTT GGCACCAATG ATTATTCACG GCATCAAGAC  
 3701 CCAGGGTGCC CGTCAGAAGT TCTCCAGCCT CTACATCTCT CAGTTTATCA  
 3751 TCATGTATAG TCTTGATGGG AAGAAGTGGC AGACTTATCG AGGAAATTCC  
 3801 ACTGGAACCT TAATGGTCTT CTTTGGCAAT GTGGATTCAT CTGGGATAAA  
 3851 ACACAATATT TTTAACCCCTC CAATTATTGC TCGATACATC CGTTTGACCC  
 3901 CAACTCATTG TAGCATTCGC AGCACTCTTC GCATGGAGTT GATGGGCTGT  
 3951 GATTTAAATA GTTGACAGCAT GCCATTGGGA ATGGAGAGTA AAGCAATATC  
 4001 AGATGCACAG ATTACTGCTT CATCCTACTT TACCAATATG TTTGCCACCT  
 4051 GGTCTCCTTC AAAAGCTCGA CTTACCTCC AAGGGAGGAG TAATGCCTGG  
 4101 AGACCTCAGG TGAATAATCC AAAAGAGTGG CTGCAAGTGG ACTTCCAGAA  
 4151 GACAATGAAA GTCACAGGAG TAACTACTCA GGGAGTAAAA TCTCTGCTTA  
 4201 CCAGCATGTA TGTGAAGGAG TTCCTCATCT CCAGCAGTCA AGATGGCCAT  
 4251 CAGTGGACTC TCTTTTTTCA GAATGGCAA GTAAAGGTTT TTCAGGGAAA  
 4301 TCAAGACTCC TTCACACCTG TGGTGAACCTC TCTAGACCCA CCGTTACTGA  
 4351 CTCGTACCT TCGAATTCAC CCCAGAGTT GGGTGCACCA GATTGCCCTG  
 4401 AGGATGGAGG TTCTGGGCTG CGAGGCACAG GACCTCTACT GAGGGTGGCC  
 4451 ACTGCAGCAC CTGCCACTGC CGTCACCTCT CCCTCCTCAG CTCCAGGGCA  
 4501 GTGTCCCTCC CTGGCTTGCC TTCTACCTTT GTGCTAAATC CTAGCAGACA  
 4551 CTGCCTTGAA GCCTCCTGAA TTAACATCA TCAGTCCTGC ATTTCTTTGG  
 4601 TGGGGGGCCA GGAGGGTGCA TCCAATTTAA CTTAACTCTT ACCGTCGACC  
 4651 TGCAGGCCCC ACGCGGCCGC

Fig. 12

(2 of 2)

98/712214

Synthetic Factor VIII B domain deleted gene segment inserted in the expression vector

```

1  AAGCTTAAAC CATGCCCATG GGGTCTCTGC AACCGCTGGC CACCTTGTA
51 CTGCTGGGGA TGCTGGTCGC TTCCGTGCTA GCCGCCACCC GCCGCTACTA
101 CCTGGGCGCC GTGGAGCTGT CCTGGGACTA CATGCAGAGC GACCTGGGCG
151 AGCTCCCCGT GGACGCCCCG TTCCCCCCCC GCGTGCCCAA GAGCTTCCCC
201 TTCAACACCA GCGTGGTGTA CAAGAAAACC CTGTTCGTGG AGTTCACCGA
251 CCACCTGTTC AACATTGCCA AGCCGCGCCC CCCCTGGATG GGCCTGCTGG
301 GCCCCACCAT CCAGGCCGAG GTGTACGACA CCGTGGTGAT CACCCTGAAG
351 AACATGGCCA GCCACCCCGT CAGCCTGCAC GCCGTGGGCG TGAGCTACTG
401 GAAGGCGAGC GAGGGCGCCG AGTACGACGA CCAGACGTCC CAGCGCGAGA
451 AGGAGGACGA CAAGGTGTTC CCGGGGGGGA GCCACACCTA CGTGTGGCAG
501 GTGCTTAAGG AGAACGGCCC TATGGCCAGC GACCCCTGTG GCCTGACCTA
551 CAGCTACCTG AGCCACGTGG ACCTGGTGAA GGATCTGAAC AGCGGGCTGA
601 TCGGCGCCCT GCTGGTGTGT CGCGAGGGCA GCCTGGCCAA GGAGAAAACC
651 CAGACCCTGC ACAAGTTCAT CTGTCTGTTC GCCGTGTTTC ACGAGGGGAA
701 GAGCTGGCAC AGCGAGACTA AGAACAGCCT GATGCAGGAC CGCGACGCCG
751 CCAGCGCCCC CGCCTGGCCC AAGATGCACA CCGTTAACGG CTACGTGAAC
801 CGCAGCCTGC CCGGCCTGAT CGGCTGCCAC CGCAAGAGCG TGTA CTGGCA
851 CGTCATCGGC ATGGGCACCA CCCCTGAGGT GCACAGCATC TTCCTGGAGG
901 GCCACACCTT CCTGGTGGCG AACCAACGCC AGGCCAGCCT GGAGATCAGC
951 CCCATCACCT TCCTGACTGC CCAGACCCTG CTGATGGACC TAGGCCAGTT
1001 CCTGCTGTTC TGCCACATCA GCAGCCACCA GCACGACGGC ATGGAGGCTT
1051 ACGTGAAGGT GGACAGCTGC CCCGAGGAGC CCCAGCTGCG CATGAAGAAC
1101 AACGAGGAGG CCGAGGACTA CGACGACGAC CTGACCGACA GCGAGATGGA
1151 TGTCGTACGC TTCGACGACG ACAACAGCCC CAGCTTCATC CAGATCCGCA
1201 GCGTGGCCAA GAAGCACCCCT AAGACCTGGG TGCACTACAT CGCCGCCGAG
1251 GAGGAGGACT GGGACTACGC CCCGCTAGTA CTGGCCCCCG ACGACCCGAG
1301 CTACAAGAGC CAGTACCTGA ACAACGGCCC CCAGCGCATC GGCCGCAAGT
1351 ACAAGAAGGT GCGCTTCATG GCCTACACCG ACGAGACTTT CAAGACCCGC
1401 GAGGCCATCC AGCACGAGTC CGGCATCCTC GGCCCCCTGC TGTACGGCGA
1451 GGTGGGCGAC ACCCTGCTGA TCATCTTCAA GAACCAGGCC AGCAGGCCCT
1501 ACAACATCTA CCCCCACGGC ATCACCGACG TGCGCCCCCT GTACAGCCGC
1551 CGCCTGCCCA AGGGCGTGAA GCACCTGAAG GACTTCCCCA TCCTGCCCGG
1601 CGAGATCTTC AAGTACAAGT GGACCGTGAC CGTGGAGGAC GGCCCCACCA
1651 AGAGCGACCC CCGCTGCCTG ACCCGCTACT ACAGCAGCTT CGTGAACATG
1701 GAGCGCGACC TGGCCTCCGG ACTGATCGGC CCCCTGCTGA TCTGCTACAA
1751 GGAGAGCGTG GACCAGCGCG GCAACCAGAT CATGAGCGAC AAGCGCAACG
1801 TGATCCTGTT CAGCGTGTTC GACGAGAACC GCAGCTGGTA TCTGACCGAG
1851 AACATCCAGC GCTTCCTGCC CAACCCCGCT GGCGTGACG TGGAAGATCC
1901 CGAGTTCCAG GCCAGCAACA TCATGCACAG CATCAACGGC TACGTGTTCT
1951 ACAGCCTGCA GCTGAGCGTG TGCCTGCATG AGGTGGCCTA CTGGTACATC
2001 CTGAGCATCG GCGCCAGAC CGACTTCCTG AGCGTGTCT TCTCCGGGTA
2051 TACCTTCAAG CACAAGATGG TGTACGAGGA CACCCTGACC CTGTTCCCTT
2101 TCTCCGGCGA GACTGTGTTC ATGTCTATGG AGAACCCCGG CCTGTGGATT
2151 CTGGGCTGCC ACAACAGCGA CTTCGCAAC CGCGGCATGA CTGCCCTGCT
2201 GAAAGTCTCC AGCTGCGACA AGAACACCGG CGACTACTAC GAGGACAGCT
2251 ACGAGGACAT CTCCGCCTAC CTGCTGTCCA AGAACACGC CATCGAGCCC
2301 CGCTCCTTCT CCAAAACTC CCGCCACCCC AGCACGCGTC AGAAGCAGTT
2351 CAACGCCACC CCCCCGTGC TGAAGCGCCA CCAGCGCGAG ATCACCCGCA
2401 CCACCTGCA AAGCGACCAG GAGGAGATCG ACTACGACGA CACCATCAGC
2451 GTGGAGATGA AGAAGGAGGA CTTGACATC TACGACGAGG ACGAGAACCA
2501 GAGCCCCGCG TCCTTCCAAA AGAAAACCCG CCACTACTTC ATCGCCGCCG
2551 TGGAGCGCCT GTGGGACTAC GGCATGAGCA GCAGCCCCCA CGTCTGCGC
2601 AACCGCGCCC AGAGCGGCAG CGTGCCCCAG TTCAAGAAGG TGGTGTTCGA
2651 GGAGTTCACC GACGGCAGCT TCACCCAGCC CCTGTACCGC GGCGAGCTGA
2701 ACGAGCACCT GGGCCTGCTC GGCCCTACA TCCGCGCCGA GGTGGAGGAC

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Fig. 13

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2751	AACATCATGG	TGACCTTCGG	CAACCAAGCC	TCCCGGCCCT	ACTCCTTCTA
2801	CTCCTCCCTG	ATCAGCTACG	AGGAGGACCA	GCGCCAGGGC	GCCGAGCCCC
2851	GCAAGAACTT	CGTGAAGCCC	AACGAGACTA	AGACCTACTT	CTGGAAGGTG
2901	CAGCACCACA	TGGCCCCCAC	CAAGGACGAG	TTCGACTGCA	AGGCCTGGGC
2951	CTACTTCAGC	GACGTGGACC	TGGAGAAGGA	CGTGCACAGC	GGCCTGATCG
3001	GGCCCTTGCT	GGTGTGCCAC	ACCAACACCC	TGAACCCCCC	CCACGGGAGG
3051	CAGGTGACTG	TGCAGGAATT	TGCCCTGTTC	TTCACCATCT	TCGACGAGAC
3101	TAAGAGCTGG	TACTTCACCG	AGAACATGGA	GCGCAACTGC	CGCGCCCCCT
3151	GCAACATCCA	GATGGAAGAT	CCCACCTTCA	AGGAGAACTA	CCGCTTCCAC
3201	GCCATCAACG	GCTACATCAT	GGACACCCTG	CCCGGCCTGG	TGATGGCCCCA
3251	GGACCAGCGC	ATCCGCTGGT	ACCTGCTGTC	TATGGGCAGC	AACGAGAACA
3301	TCCACAGCAT	CCACTTCAGC	GGCCACGTTT	TCACCGTGCG	CAAGAAGGAG
3351	GAGTACAAGA	TGGCCCTGTA	CAACCTGTAC	CCCGGCGTGT	TCGAGACTGT
3401	GGAGATGCTG	CCCAGCAAGG	CCGGGATCTG	GCGCGTGGAG	TGCCTGATCG
3451	GCGAGCACCT	GCACGCCGGC	ATGAGCACCC	TGTTCTTGGT	GTACAGCAAC
3501	AAGTGCCAGA	CCCCCTGGG	CATGGCCAGC	GGCCACATCC	GCGACTTCCA
3551	GATCACCGCC	AGCGGCCAGT	ACGGCCAGTG	GGCTCCCAAG	CTGGCCCCGCC
3601	TGCACTACAG	CGGCAGCATC	AACGCCTGGT	CGACCAAGGA	GCCCTTCTCC
3651	TGGATCAAGG	TGGACCTGCT	GGCCCCCATG	ATCATCCACG	GCATCAAGAC
3701	CCAGGGCGCC	CGCCAGAAGT	TCAGCAGCCT	GTACATCAGC	CAGTTCATCA
3751	TCATGTACTC	TCTAGACGGC	AAGAAGTGGC	AGACCTACCG	CGGCAACAGC
3801	ACCGGCACCC	TGATGGTGTT	CTTCGGCAAC	GTGGACAGCA	GCGGCATCAA
3851	GCACAACATC	TTCAACCCCC	CCATCATCGC	CCGCTACATC	CGCCTGCACC
3901	CCACCCACTA	CAGCATCCGC	AGCACCTGTC	GCATGGAGCT	GATGGGCTGC
3951	GACCTGAACA	GCTGCAGCAT	GCCCCCTGGG	ATGGAGAGCA	AGGCCATCAG
4001	CGACGCCCAG	ATCACCGCCT	CCAGCTACTT	CACCAACATG	TTCGCCACCT
4051	GGAGCCCCAG	CAAGGCCCGC	CTGCACCTGC	AGGGCCGCAG	CAACGCCTGG
4101	CGCCCCCAGG	TGAACAACCC	CAAGGAGTGG	CTGCAGGTGG	ACTTCCAGAA
4151	AACCATGAAG	GTGACTGGCG	TGACCACCCA	GGGCGTCAAG	AGCCTGCTGA
4201	CCAGCATGTA	CGTGAAGGAG	TTCTTGATCA	GCAGCAGCCA	GGACGGCCAC
4251	CAGTGGACCC	TGTTCTTCCA	AAACGGCAAG	GTGAAGGTGT	TCCAGGGCAA
4301	CCAGGACAGC	TTACACCCGG	TCGTGAACAG	CCTGGACCCC	CCCCTGCTGA
4351	CCCGCTACCT	GCGCATCCAC	CCCCAGAGCT	GGGTGCACCA	GATCGCCCTG
4401	CGCATGGAGG	TGCTGGGCTG	CGAGGCCCCAG	GACCTGTACT	GAAGCGGCCG
4451	C				

Fig. 13

(2 of 2)



COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled HIGH LEVEL EXPRESSION OF PROTEINS, the specification of which

☐ is attached hereto.

☒ was filed on September 20, 1996 as Application Serial No. 08/717,294  
and was amended on \_\_\_\_\_.

☐ was described and claimed in PCT International Application No. \_\_\_\_\_  
filed on \_\_\_\_\_ and as amended under PCT Article 19 on \_\_\_\_\_.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Anita L. Meiklejohn, Reg. No. 35,283; Karen F. Lech, Reg. No. 35,238; William E. Booth, Reg. No. 28,933; Barry E. Bretschneider, Reg. No. 28,055; John W. Freeman, Reg. No. 29,066; Timothy A. French, Reg. No. 30,175; Alan H. Gordon, Reg. No. 26,168; John F. Land, Reg. No. 29,554; John B. Pegram, Reg. No. 25,198; Rene D. Tegtmeier, Reg. No. 33,567; Hans R. Troesch, Reg. No. 36,950; Dorothy P. Whelan, Reg. No. 33,814; Charles C. Winchester, Reg. No. 21,040.

Address all telephone calls to Anita L. Meiklejohn at telephone number 617/542-5070.

Address all correspondence to Paul T. Clark, Reg. No. 30,162, Fish & Richardson P.C., 225 Franklin Street, Boston, MA 02110-2804.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Full Name of Inventor: Brian Seed

Inventor's Signature: Brian Seed

Date: Nov. 15, 1996

Residence Address: Boston, MA

Citizen of: USA

Post Office Address: Nine Hawthorne Place, Apt. 5J, Boston, MA 02114

• **COMBINED DECLARATION AND POWER OF ATTORNEY CONTINUED**

Full Name of Inventor: Jurgen Haas

Inventor's Signature: \_\_\_\_\_

Date: \_\_\_\_\_

Residence Address: Schriesheim, Germany

Citizen of: Germany

DEX

Post Office Address: Huberweg 13, 69198 Schriesheim, Germany

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COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled HIGH LEVEL EXPRESSION OF PROTEINS, the specification of which

■ is attached hereto.

☐ was filed on \_\_\_\_\_ as Application Serial No. \_\_\_\_\_  
and was amended on \_\_\_\_\_.

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I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Anita L. Meiklejohn, Reg. No. 35,283; Karen F. Lech, Reg. No. 35,238; William E. Booth, Reg. No. 28,933; Barry E. Bretschneider, Reg. No. 28,055; John W. Freeman, Reg. No. 29,066; Timothy A. French, Reg. No. 30,175; Alan H. Gordon, Reg. No. 26,168; John F. Land, Reg. No. 29,554; John B. Pegram, Reg. No. 25,198; Rene D. Tegtmeier, Reg. No. 33,567; Hans R. Troesch, Reg. No. 36,950; Dorothy P. Whelan, Reg. No. 33,814; Charles C. Winchester, Reg. No. 21,040.

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Full Name of Inventor: Brian Seed

Inventor's Signature: \_\_\_\_\_ Date: \_\_\_\_\_

Residence Address: Boston, MA

Citizen of: USA

Post Office Address: Nine Hawthorne Place, Apt. 5J, Boston, MA 02114

# COMBINED DECLARATION AND POWER OF ATTORNEY CONTINUED

Full Name of Inventor: Jurgen Haas

Inventor's Signature: \_\_\_\_\_ Date: \_\_\_\_\_

Residence Address: Schriesheim, Germany

Citizen of: Germany

Post Office Address: Huberweg 13, 69198 Schriesheim, Germany

204382.B11



#3

PATENT  
ATTORNEY DOCKET NO. 00786/345001

Date of Deposit January 13, 1997

I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner of Patents and Trademarks, Washington, D.C. 20231.

Lisa Fothergill  
(Type or print name of person mailing paper or fee)

Lisa Fothergill  
(Signature of person mailing paper or fee)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Brian Seed et al.  
Serial No.: 08/717,294  
Filed : September 20, 1996  
Title : HIGH LEVEL EXPRESSION OF PROTEINS

Art Unit:  
Examiner:

Assistant Commissioner of Patents and Trademarks  
Washington, DC 20231

DECLARATION OF MS. SUSAN M. CUFFE

1. I am an Executive Secretary at The General Hospital Corporation, the assignee of the above-identified patent application.

2. I have made a diligent effort to reach Jurgen Haas, a named joint inventor of this application. In particular, I initially sent Dr. Haas a facsimile but received no answer. I then tried to reach Dr. Haas by telephone but was unsuccessful. Lastly, I sent Dr. Haas a package by International Federal Express. Federal Express contacted me and informed me that Dr. Haas no longer lived at that address and that no forwarding address was available.

3. The last known address of Dr. Haas was Huberweg 13, 69198 Schriesheim, Germany.

4. I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are

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punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Date: 12/31/96

Susan M. Cuffe  
Susan M. Cuffe



PATENT

ATTORNEY DOCKET NO. 00786/345001

Date of Deposit January 13, 1997  
I hereby certify under 37 CFR 1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner of Patents and Trademarks, Washington, D.C. 20231.

Lisa Fothergill  
(Type or print name of person mailing paper or fee)

Lisa Fothergill  
(Signature of person mailing paper or fee)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Brian Seed et al.

Art Unit:

Serial No.: 08/717,294

Examiner:

Filed : September 20, 1996

Title : HIGH LEVEL EXPRESSION OF PROTEINS

Assistant Commissioner of Patents and Trademarks  
Washington, DC 20231

DECLARATION OF DR. BRIAN SEED

1. I am a named inventor on the above-identified patent application.
2. As indicated in the accompanying copy of my Combined Declaration and Power of Attorney, I have declared that I am an original, first, and joint inventor of the subject matter which is claimed in this application and for which a patent is sought.
3. The other named inventor on the above-identified application, Jurgen Haas, is no longer working in my laboratory.
4. His last known address was Huberweg 13, 69198 Schriesheim, Germany.
5. It is my understanding that representatives of the General Hospital Corporation (the assignees of this application) have diligently tried to reach Dr. Haas at this address, but have been unsuccessful.
6. I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are

punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Date: December 27, 1996

Brian Seed  
Brian Seed

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